



Sequence Listing

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Baker Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
Pan, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William I.

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Pro Asn Val Ser	Glu Lys Ile Leu Ile	Asp Ile Ile Gly Val	Asp
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Phe Ala Phe Ala	Glu Leu Cys Val Val	Pro Leu Arg Ile Phe	Ser
	365	370	375
Phe Phe Pro Val	Pro Val Thr Val Arg	Ala His Leu Thr Gly	Trp
	380	385	390
Leu Met Thr Leu	Lys Lys Thr Phe Val	Leu Ala Pro Ser Ser	Val
	395	400	405
Leu Arg Ile Ile	Val Leu Ile Ala Ser	Leu Val Val Leu Pro	Tyr
	410	415	420
Leu Gly Val His	Gly Ala Thr Leu Gly	Val Gly Ser Leu Leu	Ala
	425	430	435
Gly Phe Val Gly	Glu Ser Thr Met Val	Ala Ile Ala Ala Cys	Tyr
	440	445	450
Val Tyr Arg Lys	Gln Lys Lys Lys Met	Glu Asn Glu Ser Ala	Thr
	455	460	465
Glu Gly Glu Asp	Ser Ala Met Thr Asp	Met Pro Pro Thr Glu	Glu
	470	475	480
Val Thr Asp Ile	Val Glu Met Arg Glu	Glu Asn Glu	
	485	490	

<210> 8
<211> 535
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 33, 66, 96, 387
<223> unknown base

<400> 8
cctgacagaa gtgccccgga gctgggggag atncaacatt aagaagatgc 50
tgagcttctg gtgcnttttg gctctaattc tggccacaca gagaancagt 100
cggcctattg tcaacctctt tgtttcccg gaccttggtg gcagttctgc 150
agccacagag gcagtggcga ttttgacagc cacataacct gtgggtcaca 200
tgccatacgg ctggttgacg gaaatccgtg ctgtgtatcc tgctttcgac 250
aagaataacc ccagcaacaa actggtgagc acgagcaaca cagtcacggc 300
ggcccacatc aagaagttca ccttcgtctg catggctctg tcactcacgc 350
tctgtttcgt gatgttttgg acaccaacg tgtctgngaa aatcttgata 400
gacatcatcg gagtggactt tgcctttgca gaactctgtg ttgttccttt 450
gcggatcttc tccttcttcc cagttccagt cacagtgagg gcgcatctca 500
ccgggtggct gatgacactg aagaaaacct tcgtc 535

<210> 9
<211> 434
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 32, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 228, 273,
293, 296, 305, 336, 358, 361
<223> unknown base

<400> 9
tgacggaatc ccgggctggg tatcctgggt tngacaagat aaacccccag 50
caanaaattg gggagcaggg caaaacagtn acgggcagcc cacatcaaga 100
agttcacctt ngtttgnatg gntctgtcaa ctcacgctnt gtttcgtgat 150
gttttgga cccaaagtgt ttgagaaaat tttgatagac atnatcggag 200
tggantttgc ctttgacagaa ntttgngntg ttcctttgcg gattttctcc 250
tttttcccag ttccagtcac agngagggcg catctcaccg gngngntgat 300

gacantgaag aaaacctttg tccttgcccc cagctntttg gtgcggatca 350
ttgtcctnat ngccagcctt gtggtcctac cctacctggg ggtgcacggt 400
gcgaccctgg gcgtgggttc cctcctggcg ggca 434

<210> 10
<211> 154
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 33, 49, 68, 83, 90, 98, 119
<223> unknown base

<400> 10
tattcccagt tccggtcacg gggagggcgc atntcaccgg gtggctgang 50
aactgaaga aaaccttngt ccttgcccc agntttgtgn tgcggatnat 100
cgtcctcatc gccagcctng tggtcctacc ctacctgggg gtgcacggtg 150
agac 154

<210> 11
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 11
ctgatccggt tcttggtgcc cctg 24

<210> 12
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 12
gctctgtcac tcacgctc 18

<210> 13
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 13
tcattcttcc cctctccc 18

<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 14
ccttccgcca cggagttc 18

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 15
ggcaaagtcc actccgatga tgtc 24

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 16
gcctgctgtg gtcacaggtc tccg 24

<210> 17
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 17
tcggggagca ggccttgaac cggggcattg ctgctgtcaa ggagg 45

<210> 18
<211> 1901
<212> DNA
<213> Homo sapiens

<400> 18
gccccgcgcc cggcgccggg cgcccgaagc cgggagccac cgccatgggg 50
gcctgcctgg gagcctgctc cctgctcagc tgcgcgtcct gcctctgcgg 100
ctctgcccc tgcatactgt gcagctgctg ccccgccagc cgcaactcca 150

ccgtgagccg cctcatcttc acgttcttcc tcttctggg ggtgctggtg 200
tccatcatta tgctgagccc gggcgtggag agtcagctct acaagctgcc 250
ctgggtgtgt gaggaggggg ccgggatccc caccgtcctg cagggccaca 300
tcgactgtgg ctccctgctt ggctaccgcg ctgtctaccg catgtgcttc 350
gccacggcgg ccttcttctt cttctttttc accctgctca tgctctgctg 400
gagcagcagc cgggaccccc gggctgccat ccagaatggg ttttggttct 450
ttaagttcct gatcctggtg ggctcaccg tgggtgcctt ctacatccct 500
gacggctcct tcaccaacat ctggttctac ttcggcgctg tgggctcctt 550
cctcttcac ctcattccagc tgggtgctgt catcgacttt gcgcactcct 600
ggaaccagcg gtggctgggc aaggccgagg agtgcgattc ccgtgcctgg 650
tacgcaggcc tcttcttctt cactctcttc ttctacttgc tgcgatcgc 700
ggccgtggcg ctgatgttca tgtactacac tgagcccagc ggctgccacg 750
agggcaaggt cttcatcagc ctcaacctca ccttctgtgt ctgcgtgtcc 800
atcgctgctg tcctgcccac ggtccaggac gccagccca actcgggtct 850
gctgcaggcc tcggtcatca ccctctacac catgtttgtc acctggtcag 900
ccctatccag tatccctgaa cagaaatgca accccattt gccaacccag 950
ctgggcaacg agacagttgt ggcaggcccc gagggctatg agaccagtg 1000
gtgggatgcc ccgagcattg tgggcctcat catcttcttc ctgtgcaccc 1050
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cagaccgagg agtgcccacc tatgctagac gccacacagc agcagcagca 1150
gcaggtggca gcctgtgagg gccgggcctt tgacaacgag caggacggcg 1200
tcacctacag ctactccttc ttccatttct gcctggtgct ggctcactg 1250
cacgtcatga tgacgctcac caactggtac aagcccgtg agaccggaa 1300
gatgatcagc acgtggaccg ccgtgtgggt gaagatctgt gccagctggg 1350
cagggtgct cctctacctg tggaccctgg tagccccact cctcctgcgc 1400
aaccgcgact tcagctgagg cagcctcaca gcctgccatc tgggtgcctcc 1450
tgccacctgg tgctctcgg ctcggtgaca gccaacctgc cccctcccca 1500
caccaatcag ccaggctgag ccccccccc tgccccagct ccaggacctg 1550
ccctgagcc gggccttcta gtcgtagtgc cttcagggtc cgaggagcat 1600

caggctcctg cagagcccca tcccccgcc acaccacac ggtggagctg 1650
 cctcttcctt cccctcctcc ctgttgccca tactcagcat ctcggatgaa 1700
 agggctccct tgtcctcagg ctccacggga gcggggctgc tggagagagc 1750
 ggggaactcc caccacagtg gggcatccgg cactgaagcc ctggtgttcc 1800
 tggtcacgtc cccagggga cctgcccc ttctggact tcgtgcctta 1850
 ctgagtctct aagacttttt ctaataaaca agccagtgcg tgtaaaaaaa 1900
 a 1901

<210> 19
 <211> 457
 <212> PRT
 <213> Homo sapiens

<400> 19
 Met Gly Ala Cys Leu Gly Ala Cys Ser Leu Leu Ser Cys Ala Ser
 1 5 10 15
 Cys Leu Cys Gly Ser Ala Pro Cys Ile Leu Cys Ser Cys Cys Pro
 20 25 30
 Ala Ser Arg Asn Ser Thr Val Ser Arg Leu Ile Phe Thr Phe Phe
 35 40 45
 Leu Phe Leu Gly Val Leu Val Ser Ile Ile Met Leu Ser Pro Gly
 50 55 60
 Val Glu Ser Gln Leu Tyr Lys Leu Pro Trp Val Cys Glu Glu Gly
 65 70 75
 Ala Gly Ile Pro Thr Val Leu Gln Gly His Ile Asp Cys Gly Ser
 80 85 90
 Leu Leu Gly Tyr Arg Ala Val Tyr Arg Met Cys Phe Ala Thr Ala
 95 100 105
 Ala Phe Phe Phe Phe Phe Phe Thr Leu Leu Met Leu Cys Val Ser
 110 115 120
 Ser Ser Arg Asp Pro Arg Ala Ala Ile Gln Asn Gly Phe Trp Phe
 125 130 135
 Phe Lys Phe Leu Ile Leu Val Gly Leu Thr Val Gly Ala Phe Tyr
 140 145 150
 Ile Pro Asp Gly Ser Phe Thr Asn Ile Trp Phe Tyr Phe Gly Val
 155 160 165
 Val Gly Ser Phe Leu Phe Ile Leu Ile Gln Leu Val Leu Leu Ile
 170 175 180

Asp Phe Ala His Ser Trp Asn Gln Arg Trp Leu Gly Lys Ala Glu	185	190	195
Glu Cys Asp Ser Arg Ala Trp Tyr Ala Gly Leu Phe Phe Phe Thr	200	205	210
Leu Leu Phe Tyr Leu Leu Ser Ile Ala Ala Val Ala Leu Met Phe	215	220	225
Met Tyr Tyr Thr Glu Pro Ser Gly Cys His Glu Gly Lys Val Phe	230	235	240
Ile Ser Leu Asn Leu Thr Phe Cys Val Cys Val Ser Ile Ala Ala	245	250	255
Val Leu Pro Lys Val Gln Asp Ala Gln Pro Asn Ser Gly Leu Leu	260	265	270
Gln Ala Ser Val Ile Thr Leu Tyr Thr Met Phe Val Thr Trp Ser	275	280	285
Ala Leu Ser Ser Ile Pro Glu Gln Lys Cys Asn Pro His Leu Pro	290	295	300
Thr Gln Leu Gly Asn Glu Thr Val Val Ala Gly Pro Glu Gly Tyr	305	310	315
Glu Thr Gln Trp Trp Asp Ala Pro Ser Ile Val Gly Leu Ile Ile	320	325	330
Phe Leu Leu Cys Thr Leu Phe Ile Ser Leu Arg Ser Ser Asp His	335	340	345
Arg Gln Val Asn Ser Leu Met Gln Thr Glu Glu Cys Pro Pro Met	350	355	360
Leu Asp Ala Thr Gln Gln Gln Gln Gln Gln Val Ala Ala Cys Glu	365	370	375
Gly Arg Ala Phe Asp Asn Glu Gln Asp Gly Val Thr Tyr Ser Tyr	380	385	390
Ser Phe Phe His Phe Cys Leu Val Leu Ala Ser Leu His Val Met	395	400	405
Met Thr Leu Thr Asn Trp Tyr Lys Pro Gly Glu Thr Arg Lys Met	410	415	420
Ile Ser Thr Trp Thr Ala Val Trp Val Lys Ile Cys Ala Ser Trp	425	430	435
Ala Gly Leu Leu Leu Tyr Leu Trp Thr Leu Val Ala Pro Leu Leu	440	445	450
Leu Arg Asn Arg Asp Phe Ser	455		

<210> 20
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 20
gccgcctcat cttcacgttc ttcc 24

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 21
tcatccagct ggtgctgctc 20

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 22
cttcttcac ttctgcctgg 20

<210> 23
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 23
cctgggcaaa aatgcaac 18

<210> 24
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 24
caggaatgta gaaggcacc acgg 24

<210> 25
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 25
tggcacagat cttcacccac acgg 24

<210> 26
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
tgtccatcat tatgctgagc ccgggcgtgg agagtcagct ctacaagctg 50

<210> 27
<211> 1351
<212> DNA
<213> Homo sapiens

<400> 27
gagcgaggcc ggggactgaa ggtgtgggtg tcgagccctc tggcagaggg 50
ttaacctggg tcaaatgcac ggattctcac ctctacagt tacgctctcc 100
cgcggcacgt ccgcgaggac ttgaagtctt gagcgctcaa gtttgtccgt 150
aggtcgagag aaggccatgg aggtgccgcc accggcaccg cggagctttc 200
tctgtagagc attgtgccta tttccccgag tctttgctgc cgaagctgtg 250
actgccgatt cggaagtcct tgaggagcgt cagaagcggc ttccctacgt 300
cccagagccc tattaccgag aatctggatg ggaccgcctc cgggagctgt 350
ttggcaaaga tgaacagcag agaatttcaa aggaccttgc taatatctgt 400
aagacggcag ctacagcagg catcattggc tgggtgtatg ggggaatacc 450
agcttttatt catgctaaac aacaatacat tgagcagagc caggcagaaa 500
tttatcataa ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca 550
cgaggcttca ttcgttatgg ctggcgctgg ggttgagaaa ctgcagtgtt 600
tgtgactata ttcaacacag tgaacactag tctgaatgta taccgaaata 650
aagatgcctt aagccatttt gtaattgcag gagctgtcac gggaagtctt 700
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agccttgctg ggcactcctg taggaggcct gctgatggca tttcagaagt 800

acgctggtga gactgttcag gaaagaaaac agaaggatcg aaaggcactc 850
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cctccctgag aaaattgaaa gtagtttacg ggaagatgaa cctgagaatg 950
atgctaagaa aattgaagca ctgctaaacc ttcctagaaa cccttcagta 1000
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gagagctgaa gggagctgcc atgtccgatg aatgccaaca gacaggccac 1100
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tggcttgctc ttgtcttttt cttttctttt taactaagaa tggggctggt 1200
gtactctcac ttacttatc cttaaattta aatacatact tatgtttgta 1250
ttaatctatc aatatatgca tacatggata tatccacca cctagatttt 1300
aagcagtaaa taaaacattt cgcaaaagat taaagttgaa ttttacagtt 1350
t 1351

<210> 28
<211> 285
<212> PRT
<213> Homo sapiens

<400> 28
Met Glu Val Pro Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala
1 5 10 15
Leu Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala
20 25 30
Asp Ser Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Val
35 40 45
Pro Glu Pro Tyr Tyr Pro Glu Ser Gly Trp Asp Arg Leu Arg Glu
50 55 60
Leu Phe Gly Lys Asp Glu Gln Gln Arg Ile Ser Lys Asp Leu Ala
65 70 75
Asn Ile Cys Lys Thr Ala Ala Thr Ala Gly Ile Ile Gly Trp Val
80 85 90
Tyr Gly Gly Ile Pro Ala Phe Ile His Ala Lys Gln Gln Tyr Ile
95 100 105
Glu Gln Ser Gln Ala Glu Ile Tyr His Asn Arg Phe Asp Ala Val
110 115 120
Gln Ser Ala His Arg Ala Ala Thr Arg Gly Phe Ile Arg Tyr Gly
125 130 135

Trp	Arg	Trp	Gly	Trp	Arg	Thr	Ala	Val	Phe	Val	Thr	Ile	Phe	Asn	
									140					145	150
Thr	Val	Asn	Thr	Ser	Leu	Asn	Val	Tyr	Arg	Asn	Lys	Asp	Ala	Leu	
									155					160	165
Ser	His	Phe	Val	Ile	Ala	Gly	Ala	Val	Thr	Gly	Ser	Leu	Phe	Arg	
									170					175	180
Ile	Asn	Val	Gly	Leu	Arg	Gly	Leu	Val	Ala	Gly	Gly	Ile	Ile	Gly	
									185					190	195
Ala	Leu	Leu	Gly	Thr	Pro	Val	Gly	Gly	Leu	Leu	Met	Ala	Phe	Gln	
									200					205	210
Lys	Tyr	Ala	Gly	Glu	Thr	Val	Gln	Glu	Arg	Lys	Gln	Lys	Asp	Arg	
									215					220	225
Lys	Ala	Leu	His	Glu	Leu	Lys	Leu	Glu	Glu	Trp	Lys	Gly	Arg	Leu	
									230					235	240
Gln	Val	Thr	Glu	His	Leu	Pro	Glu	Lys	Ile	Glu	Ser	Ser	Leu	Arg	
									245					250	255
Glu	Asp	Glu	Pro	Glu	Asn	Asp	Ala	Lys	Lys	Ile	Glu	Ala	Leu	Leu	
									260					265	270
Asn	Leu	Pro	Arg	Asn	Pro	Ser	Val	Ile	Asp	Lys	Gln	Asp	Lys	Asp	
									275					280	285

<210> 29

<211> 324

<212> DNA

<213> Homo sapiens

<400> 29

cggaagtccc ttgaggagcg tcagaagcgg cttccctacg tcccagagcc 50

ctattacccg gaatctggat gggaccgctc cgggagctgt ttggcaaaga 100

tgaacagcag agaatttcaa aggaccttgc taatatctgt aagacggcag 150

ctacagcagg catcattggc tgggtgtatg ggggaatacc agcttttatt 200

catgctaaac aacaatacat tgagcagagc caggcagaaa tttatcataa 250

ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca cgaggcttca 300

ttcgttcattg gctggcgccg aacc 324

<210> 30

<211> 377

<212> DNA

<213> Homo sapiens

<220>

<221> unsure
<222> 262, 330, 371
<223> unknown base

<400> 30
tcaagtttgt ccgtaggtcg agagaaggcc atggaggtgc cgccaccggc 50
accgcgggagc ttttttctgt agagcattgt gcctatttcc ccgagttttt 100
gctgccgaag ctgtgactgc cgattcggaa gtccttgagg agcgtcagaa 150
gcggtctccc tacgtcccag agccctatta cccggaattt ggatgggacc 200
gcctccggga gctgtttggc aaagatgaac agcagagaat ttcaaaggac 250
cttgctgata tntgtaagac ggcagctaca gcaggcatca ttggctgggt 300
gtatggggga ataccagctt ttattcatgn taaacaacaa tacattgagc 350
agagccaggc agaaatttat nataacc 377

<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 31
tcgtacagtt acgtctctccc 20

<210> 32
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 32
cttgaggagc gtcagaagcg 20

<210> 33
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 33
ataacgaatg aagcctcgtg 20

<210> 34
<211> 40
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

gctaatatct gtaagacggc agctacagca ggcatcattg 40

<210> 35

<211> 1819

<212> DNA

<213> Homo sapiens

<400> 35

gagccgcccgc cgcgcgcgcg ccgcgcactg cagccccagg ccccggccccc 50

ccacccacgt ctgcgttgct gccccgcctg ggccaggccc caaaggcaag 100

gacaaagcag ctgtcagga acctccgccg gagtcgaatt tacgtgcagc 150

tgccggcaac cacaggttcc aagatggttt gcgggggctt cgcgtgttcc 200

aagaactgcc tgtgcgcct caacctgctt tacaccttgg ttagtctgct 250

gctaattgga attgctgcgt ggggcattgg cttcgggctg atttccagtc 300

tccgagtggc cggcgtggtc attgcagtgg gcattcttctt gttcctgatt 350

gcttttagtgg gtctgattgg agctgtaaaa catcatcagg tgttgcattt 400

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cttgcgcttg tttagccctg aaccaggagc aacagggtca gcttctggag 500

gttggttgga acaatacggc aagtgtcga aatgacatcc agagaaatct 550

aaactgctgt gggttccgaa gtgttaacct aaatgacacc tgtctggcta 600

gctgtgttaa aagtgaccac tcgtgctcgc catgtgctcc aatcatagga 650

gaatatgctg gagaggtttt gagatttggt ggtggcattg gcctgttctt 700

cagttttaca gagatcctgg gtgtttggct gacctacaga tacaggaacc 750

agaaagaccc ccgcgcgaat cctagtgcac tcctttgatg agaaaacaag 800

gaagatttcc tttcgtatta tgatcttggt cactttctgt aattttctgt 850

taagctccat ttgccagttt aaggaaggaa acactatctg gaaaagtacc 900

ttattgatag tggaattata tatttttact ctatgtttct ctacatgttt 950

ttttctttcc gttgctgaaa aatatttgaa acttgtggtc tctgaagctc 1000

ggtggcacct ggaatttact gtattcattg tcgggcactg tccactgtgg 1050

cctttcttag catttttacc tgcagaaaaa ctttgtatgg taccactgtg 1100

ttggttatat ggtgaatctg aacgtacatc tcaactgggtat aattatatgt 1150
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 taaaatcaga aagtatgaga tcctgttatg ttaagggaaa tccaaattcc 1250
 caatTTTTTT tggTcTTTTT aggaaagatt gttgtggtaa aaagtgttag 1300
 tataaaaatg ataatttact tgtagtcttt tatgattaca ccaatgtatt 1350
 ctagaaatag ttatgtctta ggaaattgtg gtttaatttt tgactttttac 1400
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 aagtatatct atatgatctt gatattgttt tataataatt tgaagtctaa 1550
 aagactgcat ttttaaacia gttagtatta atgcgttggc ccacgtagca 1600
 aaaagatatt tgattatctt aaaaattggt aaataccgtt ttcattgaaat 1650
 ttctcagtat tgtaacagca acttgtcaaa cctaagcata tttgaatatg 1700
 atctcccata atttgaaatt gaaatcgtat tgtgtggctc tgtatatctt 1750
 gttaaaaaat taaaggacag aaacctttct ttgtgtatgc atgtttgaat 1800
 taaaagaaag taatggaag 1819

<210> 36

<211> 204

<212> PRT

<213> Homo sapiens

<400> 36

Met	Val	Cys	Gly	Gly	Phe	Ala	Cys	Ser	Lys	Asn	Cys	Leu	Cys	Ala
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Leu	Asn	Leu	Leu	Tyr	Thr	Leu	Val	Ser	Leu	Leu	Leu	Ile	Gly	Ile
				20					25					30
Ala	Ala	Trp	Gly	Ile	Gly	Phe	Gly	Leu	Ile	Ser	Ser	Leu	Arg	Val
				35					40					45
Val	Gly	Val	Val	Ile	Ala	Val	Gly	Ile	Phe	Leu	Phe	Leu	Ile	Ala
				50					55					60
Leu	Val	Gly	Leu	Ile	Gly	Ala	Val	Lys	His	His	Gln	Val	Leu	Leu
				65					70					75
Phe	Phe	Tyr	Met	Ile	Ile	Leu	Leu	Leu	Val	Phe	Ile	Val	Gln	Phe
				80					85					90
Ser	Val	Ser	Cys	Ala	Cys	Leu	Ala	Leu	Asn	Gln	Glu	Gln	Gln	Gly
				95					100					105

Gln	Leu	Leu	Glu	Val	Gly	Trp	Asn	Asn	Thr	Ala	Ser	Ala	Arg	Asn	110	115	120
Asp	Ile	Gln	Arg	Asn	Leu	Asn	Cys	Cys	Gly	Phe	Arg	Ser	Val	Asn	125	130	135
Pro	Asn	Asp	Thr	Cys	Leu	Ala	Ser	Cys	Val	Lys	Ser	Asp	His	Ser	140	145	150
Cys	Ser	Pro	Cys	Ala	Pro	Ile	Ile	Gly	Glu	Tyr	Ala	Gly	Glu	Val	155	160	165
Leu	Arg	Phe	Val	Gly	Gly	Ile	Gly	Leu	Phe	Phe	Ser	Phe	Thr	Glu	170	175	180
Ile	Leu	Gly	Val	Trp	Leu	Thr	Tyr	Arg	Tyr	Arg	Asn	Gln	Lys	Asp	185	190	195
Pro	Arg	Ala	Asn	Pro	Ser	Ala	Phe	Leu							200		

<210> 37

<211> 390

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336

<223> unknown base

<400> 37

tgattggagc tgtaaaaaan tcttcaggtg ttgtnatttt tttatatgat 50

tattctgtaa nttgtattta ttgttcagtt ttntgtatct tgcgcttggt 100

tagccntgaa ccaggagcaa cagggtcagn ttntggaggt tggttggaac 150

aatacggcaa gtgctcgaaa tgacatccag agaaatntaa actgctgtgg 200

gttccgaagt gttaacccaa atgacacctg tntggctagc tgtgttaaaa 250

gtgaccactn gtgctcgcca tgtgctccaa tcataggaga atatgctgga 300

gaggttttga gatttggttg tggcattggc ctgttnttca gttttacaga 350

gatcctgggt gtttggctga cctacagata caggaaccag 390

<210> 38

<211> 566

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 27

<223> unknown base

<400> 38

aatcccaaat tccccaattt ttttggnctt tttagggaaa gatgtgttgt 50
ggtaaaaagt gttagtataa aaatgataat ttacttgtag tcttttatga 100
ttacaccaat gtattctaga atagttatgt cttaggaaat tgtgggttaa 150
tttttgactt ttacaggtaa gtgcaaagga gaagtgggtt catgaaatgt 200
tctaattgat aataacattt accttcagcc tcccatcaga atggaacgag 250
ttttgagtaa tccaggaagt atatctatat gatcttgata ttgttttata 300
taatttgaag tctaaaagac tgcattttta aacaagttag tattaatgcg 350
ttggcccacg tagcaaaaag atatttgatt atcttaaaaa ttgttaaata 400
ccgttttcat gaaagttctc agtattgtaa cagcaacttg tcaaacctaa 450
gcatatttga atatgatctc ccataatttg aaattgaaat cgtatttgtt 500
ggaggaaatg gcaatcttat gtgtgctgaa ggacacagta agagcaccaa 550
gttgtgcccc acttgc 566

<210> 39

<211> 264

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 84-85, 206

<223> unknown base

<400> 39

atgattatc tggtacttgt atttattgtt cagttttatg gtatcttgcg 50
cttgttttagc ccctgaaacc aggagcaaca gggnnacagc tcctggaggt 100
tggttgcaa caatcacggc caagtgactc cgcaaatgac atcccagaga 150
aatcctaaac tgctgtgggt tccgaagtgt taaccctaat gacacctgtc 200
tggtngctg tggtaaaagt gaccactcgt gctcgccatg tgctccaatc 250
ataggagaat atgc 264

<210> 40

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 40
accacgtct gcgttgctgc c 21

<210> 41
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 41
gagaatatgc tggagagg 18

<210> 42
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 42
aggaatgcac taggattcgc gcgg 24

<210> 43
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 43
ggccccaag gcaaggacaa agcagctgtc agggaaacctc cgccg 45

<210> 44
<211> 2061
<212> DNA
<213> Homo sapiens

<400> 44
cagtcaccat gaagctgggc tgtgtcctca tggcctgggc cctctacctt 50
tcccttggtg tgctctgggt ggcccagatg ctactggctg ccagttttga 100
gacgctgcag tgtgaggagc ctgtctgcac tgaggagagc agctgccaca 150
cggaggatga cttgactgat gcaaggggaag ctggcttcca ggtcaaggcc 200
tacactttca gtgaaccctt ccacctgatt gtgtcctatg actggctgat 250
cctccaaggt ccagccaagc cagtttttga aggggacctg ctggttctgc 300
gctgccaggc ctggcaagac tggccactga ctcaggtgac cttctaccga 350

gatggctcag ctctgggtcc ccccgggcct aacaggggaat tctccatcac 400
cgtggtacaa aaggcagaca gcgggcacta ccactgcagt ggcattcttc 450
agagccctgg tcttgggatc ccagaaacag catctgttgt ggctatcaca 500
gtccaagaac tgtttccagc gccaatcttc agagctgtac cctcagctga 550
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tgcagaggtc agctgcccgc ctctcttctt ccttctacaa ggatggaagg 650
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cctcatctgt atcaccagat gggccttctt ctcaaacaca tgcaggatgt 1000
gagagtctc ctcggtcacc tgctcatgga gttgaggaa ttatctggc 1050
accagaagcc tgggaccaca aaggctactg ctgaatagaa gtaaacagtt 1100
catccatgat ctacttaac caccacaata aatctgattc tttattttct 1150
cttctgtcc tgcacatatg cataagtact tttacaagtt gtcccagtgt 1200
tttgtagaa taatgtagtt aggtgagtg aaataaatt atataaagt 1250
agaattagag tttagctata attgtgtatt ctctcttaac acaacagaat 1300
tctgctgtct agatcaggaa tttctatctg ttatatcgac cagaatgttg 1350
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ggtcattata cttggggggg tgggggatgg tgggatgtgt gtctactggc 1500
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ggcagtacc cacaacgaaa aataatctgg cccaaaatgt cagttgtact 1600
gagtttgaga aaccccagcc taatgaaacc ctaggtgttg ggctctggaa 1650
tgggactttg tcccttctaa ttattatctc tttccagcct cattcagcta 1700
ttcttactga cataccagtc tttagctggg gctatggtct gttctttagt 1750
tctagtttgt atcccctcaa aagccattat gttgaaatcc taatcccaa 1800

ggtgatggca ttaagaagtg ggcctttggg aagtgattag atcaggagtg 1850
 cagagccctc atgattagga ttagtgccct tatttaaaaa ggccccagag 1900
 agctaactca cccttcacc atatgaggac gtggcaagaa gatgacatgt 1950
 atgagaacca aaaaacagct gtcgccaac accgactctg tcgttgccct 2000
 gatcttgaac ttccagcctc cagaactatg agaaataaaa ttctggttgt 2050
 ttgtagccta a 2061

<210> 45
 <211> 359
 <212> PRT
 <213> Homo sapiens

<400> 45
 Met Lys Leu Gly Cys Val Leu Met Ala Trp Ala Leu Tyr Leu Ser
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 Leu Gly Val Leu Trp Val Ala Gln Met Leu Leu Ala Ala Ser Phe
 20 25 30
 Glu Thr Leu Gln Cys Glu Gly Pro Val Cys Thr Glu Glu Ser Ser
 35 40 45
 Cys His Thr Glu Asp Asp Leu Thr Asp Ala Arg Glu Ala Gly Phe
 50 55 60
 Gln Val Lys Ala Tyr Thr Phe Ser Glu Pro Phe His Leu Ile Val
 65 70 75
 Ser Tyr Asp Trp Leu Ile Leu Gln Gly Pro Ala Lys Pro Val Phe
 80 85 90
 Glu Gly Asp Leu Leu Val Leu Arg Cys Gln Ala Trp Gln Asp Trp
 95 100 105
 Pro Leu Thr Gln Val Thr Phe Tyr Arg Asp Gly Ser Ala Leu Gly
 110 115 120
 Pro Pro Gly Pro Asn Arg Glu Phe Ser Ile Thr Val Val Gln Lys
 125 130 135
 Ala Asp Ser Gly His Tyr His Cys Ser Gly Ile Phe Gln Ser Pro
 140 145 150
 Gly Pro Gly Ile Pro Glu Thr Ala Ser Val Val Ala Ile Thr Val
 155 160 165
 Gln Glu Leu Phe Pro Ala Pro Ile Leu Arg Ala Val Pro Ser Ala
 170 175 180
 Glu Pro Gln Ala Gly Ser Pro Met Thr Leu Ser Cys Gln Thr Lys
 185 190 195

Leu	Pro	Leu	Gln	Arg	Ser	Ala	Ala	Arg	Leu	Leu	Phe	Ser	Phe	Tyr	200	205	210
Lys	Asp	Gly	Arg	Ile	Val	Gln	Ser	Arg	Gly	Leu	Ser	Ser	Glu	Phe	215	220	225
Gln	Ile	Pro	Thr	Ala	Ser	Glu	Asp	His	Ser	Gly	Ser	Tyr	Trp	Cys	230	235	240
Glu	Ala	Ala	Thr	Glu	Asp	Asn	Gln	Val	Trp	Lys	Gln	Ser	Pro	Gln	245	250	255
Leu	Glu	Ile	Arg	Val	Gln	Gly	Ala	Ser	Ser	Ser	Ala	Ala	Pro	Pro	260	265	270
Thr	Leu	Asn	Pro	Ala	Pro	Gln	Lys	Ser	Ala	Ala	Pro	Gly	Thr	Ala	275	280	285
Pro	Glu	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Pro	Pro	Pro	Thr	Pro	Ser	290	295	300
Ser	Glu	Asp	Pro	Gly	Phe	Ser	Ser	Pro	Leu	Gly	Met	Pro	Asp	Pro	305	310	315
His	Leu	Tyr	His	Gln	Met	Gly	Leu	Leu	Leu	Lys	His	Met	Gln	Asp	320	325	330
Val	Arg	Val	Leu	Leu	Gly	His	Leu	Leu	Met	Glu	Leu	Arg	Glu	Leu	335	340	345
Ser	Gly	His	Gln	Lys	Pro	Gly	Thr	Thr	Lys	Ala	Thr	Ala	Glu		350	355	

<210> 46

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 46

tgggctgtgt cctcatgg 18

<210> 47

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 47

tttccagcgc caattctc 18

<210> 48

<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 48
agttcttgga ctgtgatagc cac 23

<210> 49
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 49
aaacttggtt gtcctcagtg gctg 24

<210> 50
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 50
gtgagggacc tgtctgcact gaggagagca gctgccacac ggagg 45

<210> 51
<211> 2181
<212> DNA
<213> Homo sapiens

<400> 51
cccacgcgtc cgcccacgcg tccgcccacg ggcccgccca cgcgtccggg 50
ccaccagaag tttgagcctc tttggtagca ggaggctgga agaaaggaca 100
gaagtagctc tggctgtgat ggggatctta ctgggcctgc tactcctggg 150
gcacctaaca gtggacactt atggccgtcc catcctggaa gtgccagaga 200
gtgtaacagg accttggaag ggggatgtga atcttccctg cacctatgac 250
ccctgcaag gctacaccca agtcttggtg aagtggctgg tacaacgtgg 300
ctcagaccct gtcacatctt ttctacgtga ctcttctgga gaccatatcc 350
agcaggcaaa gtaccagggc cgcctgcatg tgagccacaa ggttccagga 400
gatgtatccc tccaattgag caccctggag atggatgacc ggagccacta 450
cacgtgtgaa gtcacctggc agactcctga tggcaaccaa gtcgtgagag 500

ataagattac tgagctccgt gtccagaaac tctctgtctc caagcccaca 550
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accttactct tcaagcctgc ggtgatagcc gactcaggct cctattttctg 750
cactgccaag ggccagggtg gctctgagca gcacagcgac attgtgaagt 800
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ggactggacc actgacatgg atggctacct tggagagacc agtgctgggc 950
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ccatttttga ccccgctcct gccctcaatt ttgattactg gcaggaaatg 1150
tggaggaagg ggggtgtggc acagacccaa tcctaaggcc ggaggccttc 1200
agggtcagga catagctgcc ttccctctct caggcacctt ctgaggttgt 1250
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ccagaatccc tgggtggtag gatcctgata attaattggc aagaattgag 1350
gcagaagggt gggaaaccag gaccacagcc ccaagtcctt tcttatgggt 1400
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caacttccca gaatctgggc aacaactact ctgatgagcc ctgcatagga 1550
caggagtacc agatcatcgc ccagatcaat ggcaactacg cccgcctgct 1600
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tcagtccttg ccttctgcat ggccttcttc cctgctacct ctcttcctgg 1750
atagcccaaa gtgtccgcct accaactctg gagccgctgg gagtcaactg 1800
ctttgccctg gaatttgcca gatgcatctc aagtaagcca gctgctggat 1850
ttggctctgg gcccttctag tatctctgcc gggggcttct ggtactcctc 1900

tctaaataacc agaggggaaga tgcccatagc actaggactt ggcatcatg 1950
 cctacagaca ctattcaact ttggcatctt gccaccagaa gacccgaggg 2000
 aggctcagct ctgccagctc agaggaccag ctatatccag gatcatttct 2050
 ctttcttcag ggccagacag cttttaattg aaattgttat ttcacaggcc 2100
 agggttcagt tctgctcctc cactataagt ctaatgttct gactctctcc 2150
 tgggtgctcaa taaatatcta atcataacag c 2181

<210> 52
 <211> 321
 <212> PRT
 <213> Homo sapiens

<400> 52
 Met Gly Ile Leu Leu Gly Leu Leu Leu Leu Gly His Leu Thr Val
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 20 25 30
 Gly Pro Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro
 35 40 45
 Leu Gln Gly Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg
 50 55 60
 Gly Ser Asp Pro Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp
 65 70 75
 His Ile Gln Gln Ala Lys Tyr Gln Gly Arg Leu His Val Ser His
 80 85 90
 Lys Val Pro Gly Asp Val Ser Leu Gln Leu Ser Thr Leu Glu Met
 95 100 105
 Asp Asp Arg Ser His Tyr Thr Cys Glu Val Thr Trp Gln Thr Pro
 110 115 120
 Asp Gly Asn Gln Val Val Arg Asp Lys Ile Thr Glu Leu Arg Val
 125 130 135
 Gln Lys Leu Ser Val Ser Lys Pro Thr Val Thr Thr Gly Ser Gly
 140 145 150
 Tyr Gly Phe Thr Val Pro Gln Gly Met Arg Ile Ser Leu Gln Cys
 155 160 165
 Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile Trp Tyr Lys Gln
 170 175 180
 Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr Leu Ser Thr
 185 190 195

Leu	Leu	Phe	Lys	Pro	Ala	Val	Ile	Ala	Asp	Ser	Gly	Ser	Tyr	Phe	200	205	210
Cys	Thr	Ala	Lys	Gly	Gln	Val	Gly	Ser	Glu	Gln	His	Ser	Asp	Ile	215	220	225
Val	Lys	Phe	Val	Val	Lys	Asp	Ser	Ser	Lys	Leu	Leu	Lys	Thr	Lys	230	235	240
Thr	Glu	Ala	Pro	Thr	Thr	Met	Thr	Tyr	Pro	Leu	Lys	Ala	Thr	Ser	245	250	255
Thr	Val	Lys	Gln	Ser	Trp	Asp	Trp	Thr	Thr	Asp	Met	Asp	Gly	Tyr	260	265	270
Leu	Gly	Glu	Thr	Ser	Ala	Gly	Pro	Gly	Lys	Ser	Leu	Pro	Val	Phe	275	280	285
Ala	Ile	Ile	Leu	Ile	Ile	Ser	Leu	Cys	Cys	Met	Val	Val	Phe	Thr	290	295	300
Met	Ala	Tyr	Ile	Met	Leu	Cys	Arg	Lys	Thr	Ser	Gln	Gln	Glu	His	305	310	315
Val	Tyr	Glu	Ala	Ala	Arg										320		

<210> 53
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 53
 tatccctcca attgagcacc ctgg 24

<210> 54
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 54
 gtcggaagac atccaacaa g 21

<210> 55
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 55
cttcacaatg tcgctgtgct gctc 24

<210> 56
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 56
agccaaatcc agcagctggc ttac 24

<210> 57
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 57
tggatgaccg gagccactac acgtgtgaag tcacctggca gactcctgat 50

<210> 58
<211> 2458
<212> DNA
<213> Homo sapiens

<400> 58
gcgccgggag cccatctgcc cccaggggca cggggcgcg ggccgggtcc 50
cgcccggcac atggctgcag ccacctcgcg cgcacccga ggcgcccgc 100
ccagctcgcc cgaggtccgt cggaggcgcc cggccgcccc ggagccaagc 150
agcaactgag cggggaagcg cccgcgtccg gggatcgga tgtccctcct 200
ccttctctc ttgctagttt cctactatgt tggaaacctg gggactcaca 250
ctgagatcaa gagagtggca gaggaaaagg tcactttgcc ctgccaccat 300
caactggggc ttccagaaaa agacactctg gatattgaat ggctgctcac 350
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aatttcctgg caggagatgc ctccttgag attgaacctc tgaagcccag 500
tgatgagggc cggtagacct gtaagggtta gaattcaggg cgctacgtgt 550
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gtcatcctct ggcacagagc ccattgtgta ttactggcag cgaatccgag 700
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ccagaggtga gaggttctga accaaagaaa gtccaccatg ctaatctgac 1250
caaagcagaa accacacca gcatgatccc cagccagagc agagccttcc 1300
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ccagatgaga ggtcatctaa gtagcagtga gcattgcacg gaacagattc 1450
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gattcatctg taaaaaggca tcttattgtg ctttagacc agagtaaggg 1550
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taaattttct atgcatttct gcaaacttat tggattatta gttattcaga 1750
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ctaactctac tatttgtatt gagcccaaaa taactatgaa aggagacaaa 2000
aatttgtgac aaaggattgt gaagagcttt ccatcttcat gatgttatga 2050
ggattgttga caaacattag aaatatataa tggagcaatt gtggatttcc 2100

cctcaaatca gatgcctcta aggactttcc tgctagatat ttctggaagg 2150
 agaaaataca acatgtcatt tatcaacgtc cttagaaaga attcttctag 2200
 agaaaaaggg atctaggaat gctgaaagat tacccaacat accattatag 2250
 tctcttcttt ctgagaaaat gtgaaaccag aattgcaaga ctgggtggac 2300
 tagaaagggg gattagatca gttttctctt aatatgtcaa ggaaggtagc 2350
 cgggcatggg gccaggcacc tgtaggaaaa tccagcaggt ggaggttgca 2400
 gtgagccgag attatgccat tgcactccag cctgggtgac agagcgggac 2450
 tccgtctc 2458

<210> 59
 <211> 373
 <212> PRT
 <213> Homo sapiens

<400> 59
 Met Ser Leu Leu Leu Leu Leu Leu Val Ser Tyr Tyr Val Gly
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 Thr Leu Gly Thr His Thr Glu Ile Lys Arg Val Ala Glu Glu Lys
 20 25 30
 Val Thr Leu Pro Cys His His Gln Leu Gly Leu Pro Glu Lys Asp
 35 40 45
 Thr Leu Asp Ile Glu Trp Leu Leu Thr Asp Asn Glu Gly Asn Gln
 50 55 60
 Lys Val Val Ile Thr Tyr Ser Ser Arg His Val Tyr Asn Asn Leu
 65 70 75
 Thr Glu Glu Gln Lys Gly Arg Val Ala Phe Ala Ser Asn Phe Leu
 80 85 90
 Ala Gly Asp Ala Ser Leu Gln Ile Glu Pro Leu Lys Pro Ser Asp
 95 100 105
 Glu Gly Arg Tyr Thr Cys Lys Val Lys Asn Ser Gly Arg Tyr Val
 110 115 120
 Trp Ser His Val Ile Leu Lys Val Leu Val Arg Pro Ser Lys Pro
 125 130 135
 Lys Cys Glu Leu Glu Gly Glu Leu Thr Glu Gly Ser Asp Leu Thr
 140 145 150
 Leu Gln Cys Glu Ser Ser Ser Gly Thr Glu Pro Ile Val Tyr Tyr
 155 160 165
 Trp Gln Arg Ile Arg Glu Lys Glu Gly Glu Asp Glu Arg Leu Pro

	170	175	180
Pro Lys Ser Arg	Ile Asp Tyr Asn His	Pro Gly Arg Val	Leu Leu
	185	190	195
Gln Asn Leu Thr	Met Ser Tyr Ser Gly	Leu Tyr Gln Cys Thr	Ala
	200	205	210
Gly Asn Glu Ala	Gly Lys Glu Ser Cys	Val Val Arg Val Thr	Val
	215	220	225
Gln Tyr Val Gln	Ser Ile Gly Met Val	Ala Gly Ala Val Thr	Gly
	230	235	240
Ile Val Ala Gly	Ala Leu Leu Ile Phe	Leu Leu Val Trp Leu	Leu
	245	250	255
Ile Arg Arg Lys	Asp Lys Glu Arg Tyr	Glu Glu Glu Glu Arg	Pro
	260	265	270
Asn Glu Ile Arg	Glu Asp Ala Glu Ala	Pro Lys Ala Arg Leu	Val
	275	280	285
Lys Pro Ser Ser	Ser Ser Ser Gly Ser	Arg Ser Ser Arg Ser	Gly
	290	295	300
Ser Ser Ser Thr	Arg Ser Thr Ala Asn	Ser Ala Ser Arg Ser	Gln
	305	310	315
Arg Thr Leu Ser	Thr Asp Ala Ala Pro	Gln Pro Gly Leu Ala	Thr
	320	325	330
Gln Ala Tyr Ser	Leu Val Gly Pro Glu	Val Arg Gly Ser Glu	Pro
	335	340	345
Lys Lys Val His	His Ala Asn Leu Thr	Lys Ala Glu Thr Thr	Pro
	350	355	360
Ser Met Ile Pro	Ser Gln Ser Arg Ala	Phe Gln Thr Val	
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<211> 24

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 60

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<210> 61

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 61

actaggctgt atgcctgggt gggc 24

<210> 62

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 62

gtatgtacaa agcatcggca tggttgcagg agcagtgaca ggc 43

<210> 63

<211> 3534

<212> DNA

<213> Homo sapiens

<400> 63

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<210> 64

<211> 655

<212> PRT

<213> Homo sapiens

<400> 64

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Leu	Leu	Leu	Gly	Phe	Leu	Ser	Thr	Thr	Thr	Ala	Gln	Pro	Glu	Gln		35	40	45	
Lys	Ala	Ser	Asn	Leu	Ile	Gly	Thr	Tyr	Arg	His	Val	Asp	Arg	Ala		50	55	60	
Thr	Gly	Gln	Val	Leu	Thr	Cys	Asp	Lys	Cys	Pro	Ala	Gly	Thr	Tyr		65	70	75	
Val	Ser	Glu	His	Cys	Thr	Asn	Thr	Ser	Leu	Arg	Val	Cys	Ser	Ser		80	85	90	
Cys	Pro	Val	Gly	Thr	Phe	Thr	Arg	His	Glu	Asn	Gly	Ile	Glu	Lys		95	100	105	
Cys	His	Asp	Cys	Ser	Gln	Pro	Cys	Pro	Trp	Pro	Met	Ile	Glu	Lys		110	115	120	
Leu	Pro	Cys	Ala	Ala	Leu	Thr	Asp	Arg	Glu	Cys	Thr	Cys	Pro	Pro		125	130	135	
Gly	Met	Phe	Gln	Ser	Asn	Ala	Thr	Cys	Ala	Pro	His	Thr	Val	Cys		140	145	150	
Pro	Val	Gly	Trp	Gly	Val	Arg	Lys	Lys	Gly	Thr	Glu	Thr	Glu	Asp		155	160	165	
Val	Arg	Cys	Lys	Gln	Cys	Ala	Arg	Gly	Thr	Phe	Ser	Asp	Val	Pro		170	175	180	
Ser	Ser	Val	Met	Lys	Cys	Lys	Ala	Tyr	Thr	Asp	Cys	Leu	Ser	Gln		185	190	195	
Asn	Leu	Val	Val	Ile	Lys	Pro	Gly	Thr	Lys	Glu	Thr	Asp	Asn	Val		200	205	210	
Cys	Gly	Thr	Leu	Pro	Ser	Phe	Ser	Ser	Ser	Thr	Ser	Pro	Ser	Pro		215	220	225	
Gly	Thr	Ala	Ile	Phe	Pro	Arg	Pro	Glu	His	Met	Glu	Thr	His	Glu		230	235	240	
Val	Pro	Ser	Ser	Thr	Tyr	Val	Pro	Lys	Gly	Met	Asn	Ser	Thr	Glu		245	250	255	
Ser	Asn	Ser	Ser	Ala	Ser	Val	Arg	Pro	Lys	Val	Leu	Ser	Ser	Ile		260	265	270	
Gln	Glu	Gly	Thr	Val	Pro	Asp	Asn	Thr	Ser	Ser	Ala	Arg	Gly	Lys		275	280	285	

Glu Asp Val Asn	Lys Thr Leu Pro Asn	Leu Gln Val Val Asn	His
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Gln Gln Gly Pro	His His Arg His Ile	Leu Lys Leu Leu Pro	Ser
305		310	315
Met Glu Ala Thr	Gly Gly Glu Lys Ser	Ser Thr Pro Ile Lys	Gly
320		325	330
Pro Lys Arg Gly	His Pro Arg Gln Asn	Leu His Lys His Phe	Asp
335		340	345
Ile Asn Glu His	Leu Pro Trp Met Ile	Val Leu Phe Leu Leu	Leu
350		355	360
Val Leu Val Val	Ile Val Val Cys Ser	Ile Arg Lys Ser Ser	Arg
365		370	375
Thr Leu Lys Lys	Gly Pro Arg Gln Asp	Pro Ser Ala Ile Val	Glu
380		385	390
Lys Ala Gly Leu	Lys Lys Ser Met Thr	Pro Thr Gln Asn Arg	Glu
395		400	405
Lys Trp Ile Tyr	Tyr Cys Asn Gly His	Gly Ile Asp Ile Leu	Lys
410		415	420
Leu Val Ala Ala	Gln Val Gly Ser Gln	Trp Lys Asp Ile Tyr	Gln
425		430	435
Phe Leu Cys Asn	Ala Ser Glu Arg Glu	Val Ala Ala Phe Ser	Asn
440		445	450
Gly Tyr Thr Ala	Asp His Glu Arg Ala	Tyr Ala Ala Leu Gln	His
455		460	465
Trp Thr Ile Arg	Gly Pro Glu Ala Ser	Leu Ala Gln Leu Ile	Ser
470		475	480
Ala Leu Arg Gln	His Arg Arg Asn Asp	Val Val Glu Lys Ile	Arg
485		490	495
Gly Leu Met Glu	Asp Thr Thr Gln Leu	Glu Thr Asp Lys Leu	Ala
500		505	510
Leu Pro Met Ser	Pro Ser Pro Leu Ser	Pro Ser Pro Ile Pro	Ser
515		520	525
Pro Asn Ala Lys	Leu Glu Asn Ser Ala	Leu Leu Thr Val Glu	Pro
530		535	540
Ser Pro Gln Asp	Lys Asn Lys Gly Phe	Phe Val Asp Glu Ser	Glu
545		550	555
Pro Leu Leu Arg	Cys Asp Ser Thr Ser	Ser Gly Ser Ser Ala	Leu
560		565	570

Ser	Arg	Asn	Gly	Ser	Phe	Ile	Thr	Lys	Glu	Lys	Lys	Asp	Thr	Val
				575					580					585
Leu	Arg	Gln	Val	Arg	Leu	Asp	Pro	Cys	Asp	Leu	Gln	Pro	Ile	Phe
				590					595					600
Asp	Asp	Met	Leu	His	Phe	Leu	Asn	Pro	Glu	Glu	Leu	Arg	Val	Ile
				605					610					615
Glu	Glu	Ile	Pro	Gln	Ala	Glu	Asp	Lys	Leu	Asp	Arg	Leu	Phe	Glu
				620					625					630
Ile	Ile	Gly	Val	Lys	Ser	Gln	Glu	Ala	Ser	Gln	Thr	Leu	Leu	Asp
				635					640					645
Ser	Val	Tyr	Ser	His	Leu	Pro	Asp	Leu	Leu					
				650					655					

<210> 65

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 65

gtagcagtgc acatgggggtg ttgg 24

<210> 66

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 66

accgcacatc ctcaagtctct gtcc 24

<210> 67

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 67

acgatgatcg cgggctccct tctcctgctt ggatttcotta gcaccaccac 50

<210> 68

<211> 2412

<212> DNA

<213> Homo sapiens

<400> 68

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<210> 69

<211> 453

<212> PRT

<213> Homo sapiens

<400> 69

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Arg	Ser	Leu	Phe	Gly	Leu	Asp	Asp	Leu	Lys	Ile	Ser	Pro	Val	Ala
				20					25					30

Pro	Asp	Ala	Asp	Ala	Val	Ala	Ala	Gln	Ile	Leu	Ser	Leu	Leu	Pro
				35				40						45

Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile

	50		55		60
Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly	65		70		75
Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala	80		85		90
Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr	95		100		105
Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe	110		115		120
Thr Ala Ala Ser Trp Lys Thr Met Cys Ser Asp Asp Trp Lys Gly	125		130		135
His Tyr Ala Asn Val Ala Cys Ala Gln Leu Gly Phe Pro Ser Tyr	140		145		150
Val Ser Ser Asp Asn Leu Arg Val Ser Ser Leu Glu Gly Gln Phe	155		160		165
Arg Glu Glu Phe Val Ser Ile Asp His Leu Leu Pro Asp Asp Lys	170		175		180
Val Thr Ala Leu His His Ser Val Tyr Val Arg Glu Gly Cys Ala	185		190		195
Ser Gly His Val Val Thr Leu Gln Cys Thr Ala Cys Gly His Arg	200		205		210
Arg Gly Tyr Ser Ser Arg Ile Val Gly Gly Asn Met Ser Leu Leu	215		220		225
Ser Gln Trp Pro Trp Gln Ala Ser Leu Gln Phe Gln Gly Tyr His	230		235		240
Leu Cys Gly Gly Ser Val Ile Thr Pro Leu Trp Ile Ile Thr Ala	245		250		255
Ala His Cys Val Tyr Asp Leu Tyr Leu Pro Lys Ser Trp Thr Ile	260		265		270
Gln Val Gly Leu Val Ser Leu Leu Asp Asn Pro Ala Pro Ser His	275		280		285
Leu Val Glu Lys Ile Val Tyr His Ser Lys Tyr Lys Pro Lys Arg	290		295		300
Leu Gly Asn Asp Ile Ala Leu Met Lys Leu Ala Gly Pro Leu Thr	305		310		315
Phe Asn Glu Met Ile Gln Pro Val Cys Leu Pro Asn Ser Glu Glu	320		325		330
Asn Phe Pro Asp Gly Lys Val Cys Trp Thr Ser Gly Trp Gly Ala					

	335	340	345
Thr Glu Asp Gly	Gly Asp Ala Ser Pro	Val Leu Asn His Ala	Ala
	350	355	360
Val Pro Leu Ile	Ser Asn Lys Ile Cys	Asn His Arg Asp	Val Tyr
	365	370	375
Gly Gly Ile Ile	Ser Pro Ser Met Leu	Cys Ala Gly Tyr Leu	Thr
	380	385	390
Gly Gly Val Asp	Ser Cys Gln Gly Asp	Ser Gly Gly Pro Leu	Val
	395	400	405
Cys Gln Glu Arg	Arg Leu Trp Lys Leu	Val Gly Ala Thr Ser	Phe
	410	415	420
Gly Ile Gly Cys	Ala Glu Val Asn Lys	Pro Gly Val Tyr Thr	Arg
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Val Thr Ser Phe	Leu Asp Trp Ile His	Glu Gln Met Glu Arg	Asp
	440	445	450

Leu Lys Thr

<210> 70

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 70

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<210> 71

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 71

tacacgtccc tgtggttgca gatc 24

<210> 72

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 72

cgttcaatgc agaaatgata cagcctgtgt gcctgcccaa ctctgaagag 50

<210> 73

<211> 3305

<212> DNA

<213> Homo sapiens

<400> 73

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<210> 74

<211> 735

<212> PRT

<213> Homo sapiens

<400> 74

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Leu	Ala	Leu	Ala	Gly	Ala	Leu	Leu	Ala	Pro	Cys	Glu	Ala	Arg	Gly	20	25	30	
Val	Ser	Leu	Trp	Asn	Gln	Gly	Arg	Ala	Asp	Glu	Val	Val	Ser	Ala	35	40	45	
Ser	Val	Arg	Ser	Gly	Asp	Leu	Trp	Ile	Pro	Val	Lys	Ser	Phe	Asp	50	55	60	
Ser	Lys	Asn	His	Pro	Glu	Val	Leu	Asn	Ile	Arg	Leu	Gln	Arg	Glu	65	70	75	
Ser	Lys	Glu	Leu	Ile	Ile	Asn	Leu	Glu	Arg	Asn	Glu	Gly	Leu	Ile	80	85	90	
Ala	Ser	Ser	Phe	Thr	Glu	Thr	His	Tyr	Leu	Gln	Asp	Gly	Thr	Asp	95	100	105	
Val	Ser	Leu	Ala	Arg	Asn	Tyr	Thr	Gly	His	Cys	Tyr	Tyr	His	Gly	110	115	120	

His Val Arg Gly Tyr Ser Asp Ser Ala Val Ser Leu Ser Thr Cys	125	130	135
Ser Gly Leu Arg Gly Leu Ile Val Phe Glu Asn Glu Ser Tyr Val	140	145	150
Leu Glu Pro Met Lys Ser Ala Thr Asn Arg Tyr Lys Leu Phe Pro	155	160	165
Ala Lys Lys Leu Lys Ser Val Arg Gly Ser Cys Gly Ser His His	170	175	180
Asn Thr Pro Asn Leu Ala Ala Lys Asn Val Phe Pro Pro Pro Ser	185	190	195
Gln Thr Trp Ala Arg Arg His Lys Arg Glu Thr Leu Lys Ala Thr	200	205	210
Lys Tyr Val Glu Leu Val Ile Val Ala Asp Asn Arg Glu Phe Gln	215	220	225
Arg Gln Gly Lys Asp Leu Glu Lys Val Lys Gln Arg Leu Ile Glu	230	235	240
Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro Leu Asn Ile Arg	245	250	255
Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met Asp Lys Cys	260	265	270
Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe Leu Asp	275	280	285
Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn Ala	290	295	300
Gln Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met	305	310	315
Ala Pro Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly Ile	320	325	330
Val Met Asp His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr Leu	335	340	345
Ala His Glu Leu Gly His Asn Phe Gly Met Asn His Asp Thr Leu	350	355	360
Asp Arg Gly Cys Ser Cys Gln Met Ala Val Glu Lys Gly Gly Cys	365	370	375
Ile Met Asn Ala Ser Thr Gly Tyr Pro Phe Pro Met Val Phe Ser	380	385	390
Ser Cys Ser Arg Lys Asp Leu Glu Thr Ser Leu Glu Lys Gly Met	395	400	405

Gly Val Cys Leu Phe Asn Leu Pro Glu Val Arg Glu Ser Phe Gly	410	415	420
Gly Gln Lys Cys Gly Asn Arg Phe Val Glu Glu Gly Glu Glu Cys	425	430	435
Asp Cys Gly Glu Pro Glu Glu Cys Met Asn Arg Cys Cys Asn Ala	440	445	450
Thr Thr Cys Thr Leu Lys Pro Asp Ala Val Cys Ala His Gly Leu	455	460	465
Cys Cys Glu Asp Cys Gln Leu Lys Pro Ala Gly Thr Ala Cys Arg	470	475	480
Asp Ser Ser Asn Ser Cys Asp Leu Pro Glu Phe Cys Thr Gly Ala	485	490	495
Ser Pro His Cys Pro Ala Asn Val Tyr Leu His Asp Gly His Ser	500	505	510
Cys Gln Asp Val Asp Gly Tyr Cys Tyr Asn Gly Ile Cys Gln Thr	515	520	525
His Glu Gln Gln Cys Val Thr Leu Trp Gly Pro Gly Ala Lys Pro	530	535	540
Ala Pro Gly Ile Cys Phe Glu Arg Val Asn Ser Ala Gly Asp Pro	545	550	555
Tyr Gly Asn Cys Gly Lys Val Ser Lys Ser Ser Phe Ala Lys Cys	560	565	570
Glu Met Arg Asp Ala Lys Cys Gly Lys Ile Gln Cys Gln Gly Gly	575	580	585
Ala Ser Arg Pro Val Ile Gly Thr Asn Ala Val Ser Ile Glu Thr	590	595	600
Asn Ile Pro Leu Gln Gln Gly Gly Arg Ile Leu Cys Arg Gly Thr	605	610	615
His Val Tyr Leu Gly Asp Asp Met Pro Asp Pro Gly Leu Val Leu	620	625	630
Ala Gly Thr Lys Cys Ala Asp Gly Lys Ile Cys Leu Asn Arg Gln	635	640	645
Cys Gln Asn Ile Ser Val Phe Gly Val His Glu Cys Ala Met Gln	650	655	660
Cys His Gly Arg Gly Val Cys Asn Asn Arg Lys Asn Cys His Cys	665	670	675
Glu Ala His Trp Ala Pro Pro Phe Cys Asp Lys Phe Gly Phe Gly	680	685	690

Gly Ser Thr Asp Ser Gly Pro Ile Arg Gln Ala Glu Ala Arg Gln
695 700 705

Glu Ala Ala Glu Ser Asn Arg Glu Arg Gly Gln Gly Gln Glu Pro
710 715 720

Val Gly Ser Gln Glu His Ala Ser Thr Ala Ser Leu Thr Leu Ile
725 730 735

<210> 75

<211> 483

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 94, 143, 156, 163, 179, 193, 369, 371, 381, 390, 473

<223> unknown base

<400> 75

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ctgacaacga aaacaaaaca gttttggggg ttcaggaggg gaantccagc 100

ctacccagga agtttgcaga aacagtgcaa ggaagggcag ganttcctgg 150

ttgagntttt tgntaaaaca tggacatgnt tcagtgtctgc tcntgagaga 200

gtagcaggtt accacttttg gcaggcccca gccctgcagc aaggaggaag 250

aggactcaaa agtttggcct ttcactgagc ctccacagca gtgggggaga 300

agcaagggtt gggcccagtg tcccctttcc ccagtgcacac ctcagccttg 350

gcagccctga taactggtnt ntggctgcaa nttaatgctn tgatatggct 400

tttagcattt attatatgaa aatagcaggg ttttagtttt taatttatca 450

gagaccctgc caccattcc atntccatcc aag 483

<210> 76

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 76

gtctcagcac gtgttctggt ctcaggg 27

<210> 77

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 77
catgagcatg tgcacggc 18

<210> 78
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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 78
tacctgcacg atgggcac 18

<210> 79
<211> 18
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 79
cactgggcac ctcccttc 18

<210> 80
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 80
ctccaggctg gtctccaagt ccttcc 26

<210> 81
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 81
tccctgttgg actctgcagc ttcc 24

<210> 82
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 82
cttcgctggg aagagtttg 19

<210> 83
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 83
gtgcaaccaa cagatacaaa ctcttcccag cgaagaagct gaaaagcgtc 50

<210> 84
<211> 1714
<212> DNA
<213> Homo sapiens

<400> 84
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atgatctgcc cgctcggcc tcccaaagtg ctgggattac aggcgagtgc 150
aaccacaccc ggccacaaac tttttaagaa gttaatgaaa ccataccttt 200
tacatTTTTa atgacaggaa aatgctcaca ataattgtta acccaaaatt 250
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<210> 85
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 85
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 20 25 30
 Thr Ser Met Pro Glu Ala Thr Ala Ala Glu Thr Thr Lys Pro Ser
 35 40 45
 Asn Ser Ala Leu Gln Pro Thr Ala Gly Leu Leu Val Val Leu Leu
 50 55 60
 Ala Leu Leu His Leu Tyr His
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<210> 86
 <211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 86

acgggcacac tggatcccaa atg 23

<210> 87

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 87

ggtagagatg tagaaggcca agcaagacc 29

<210> 88

<211> 50

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 88

gctccctacc cgtgcaggtt tcttcatttg ttcctttaac cagtatgccg 50

<210> 89

<211> 2956

<212> DNA

<213> Homo sapiens

<400> 89

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cgctctctcc cgctgctggc ccggccggcg gccctgactg cgctgctgct 100

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ggacaggacc cgcacagcaa gcacctgtac acggccgaca tggtcacgca 250

cgggatccag agcgcgcgcg acttcgtcat gttcttcgcg ccctgggtgtg 300

gacactgcca gcggctgcag ccgacttggg atgacctggg agacaaatac 350

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<210> 90

<211> 432

<212> PRT

<213> Homo sapiens

<400> 90

Met	Pro	Ala	Arg	Pro	Gly	Arg	Leu	Leu	Pro	Leu	Leu	Ala	Arg	Pro
1				5					10					15

Ala	Ala	Leu	Thr	Ala	Leu	Leu	Leu	Leu	Leu	Gly	His	Gly	Gly
				20				25					30

Gly	Gly	Arg	Trp	Gly	Ala	Arg	Ala	Gln	Glu	Ala	Ala	Ala	Ala	Ala
				35				40						45

Ala Asp Gly Pro Pro Ala Ala Asp Gly Glu Asp Gly Gln Asp Pro	50	55	60
His Ser Lys His Leu Tyr Thr Ala Asp Met Phe Thr His Gly Ile	65	70	75
Gln Ser Ala Ala His Phe Val Met Phe Phe Ala Pro Trp Cys Gly	80	85	90
His Cys Gln Arg Leu Gln Pro Thr Trp Asn Asp Leu Gly Asp Lys	95	100	105
Tyr Asn Ser Met Glu Asp Ala Lys Val Tyr Val Ala Lys Val Asp	110	115	120
Cys Thr Ala His Ser Asp Val Cys Ser Ala Gln Gly Val Arg Gly	125	130	135
Tyr Pro Thr Leu Lys Leu Phe Lys Pro Gly Gln Glu Ala Val Lys	140	145	150
Tyr Gln Gly Pro Arg Asp Phe Gln Thr Leu Glu Asn Trp Met Leu	155	160	165
Gln Thr Leu Asn Glu Glu Pro Val Thr Pro Glu Pro Glu Val Glu	170	175	180
Pro Pro Ser Ala Pro Glu Leu Lys Gln Gly Leu Tyr Glu Leu Ser	185	190	195
Ala Ser Asn Phe Glu Leu His Val Ala Gln Gly Asp His Phe Ile	200	205	210
Lys Phe Phe Ala Pro Trp Cys Gly His Cys Lys Ala Leu Ala Pro	215	220	225
Thr Trp Glu Gln Leu Ala Leu Gly Leu Glu His Ser Glu Thr Val	230	235	240
Lys Ile Gly Lys Val Asp Cys Thr Gln His Tyr Glu Leu Cys Ser	245	250	255
Gly Asn Gln Val Arg Gly Tyr Pro Thr Leu Leu Trp Phe Arg Asp	260	265	270
Gly Lys Lys Val Asp Gln Tyr Lys Gly Lys Arg Asp Leu Glu Ser	275	280	285
Leu Arg Glu Tyr Val Glu Ser Gln Leu Gln Arg Thr Glu Thr Gly	290	295	300
Ala Thr Glu Thr Val Thr Pro Ser Glu Ala Pro Val Leu Ala Ala	305	310	315
Glu Pro Glu Ala Asp Lys Gly Thr Val Leu Ala Leu Thr Glu Asn	320	325	330

Asn	Phe	Asp	Asp	Thr	Ile	Ala	Glu	Gly	Ile	Thr	Phe	Ile	Lys	Phe	
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Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Thr	Leu	Ala	Pro	Thr	Trp	
				350					355					360	
Glu	Glu	Leu	Ser	Lys	Lys	Glu	Phe	Pro	Gly	Leu	Ala	Gly	Val	Lys	
				365					370					375	
Ile	Ala	Glu	Val	Asp	Cys	Thr	Ala	Glu	Arg	Asn	Ile	Cys	Ser	Lys	
				380					385					390	
Tyr	Ser	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Leu	Phe	Arg	Gly	Gly	
				395					400					405	
Lys	Lys	Val	Ser	Glu	His	Ser	Gly	Gly	Arg	Asp	Leu	Asp	Ser	Leu	
				410					415					420	
His	Arg	Phe	Val	Leu	Ser	Gln	Ala	Lys	Asp	Glu	Leu				
				425					430						

<210> 91
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 91
 atgttccttcg cgccctggtg 20

<210> 92
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 92
 ccaagccaac acactctaca g 21

<210> 93
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 93
 aagtgtcgc cttgtgcaac gtgc 24

<210> 94
 <211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 94

ggtcaaaggg gatatatcgc cac 23

<210> 95

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 95

gcatggaaga tgccaaagtc tatgtggcta aagtggactg cacggccca 49

<210> 96

<211> 1016

<212> DNA

<213> Homo sapiens

<400> 96

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gtctggatat tgatagccgt cctaccgctg aagtctgtgc cacacacaca 150

atthcaccag gacccaaagg agatgatggg gaaaaaggag atccaggaga 200

agagggaaaag catggcaaag tgggacgcat ggggcccgaag ggaattaaag 250

gagaactggg tgatatggga gatcagggca atattggcaa gactgggccc 300

attgggaaga agggtgacaa aggggaaaaa ggthtgcttg gaatacctgg 350

agaaaaaggc aaagcaggta ctgtctgtga ttgtggaaga taccggaaat 400

ttgttggaaca actggatatt agtattgctc ggctcaagac atctatgaag 450

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<210> 97
 <211> 277
 <212> PRT
 <213> Homo sapiens

<400> 97
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 20 25 30
 Asp Ser Arg Pro Thr Ala Glu Val Cys Ala Thr His Thr Ile Ser
 35 40 45
 Pro Gly Pro Lys Gly Asp Asp Gly Glu Lys Gly Asp Pro Gly Glu
 50 55 60
 Glu Gly Lys His Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile
 65 70 75
 Lys Gly Glu Leu Gly Asp Met Gly Asp Gln Gly Asn Ile Gly Lys
 80 85 90
 Thr Gly Pro Ile Gly Lys Lys Gly Asp Lys Gly Glu Lys Gly Leu
 95 100 105
 Leu Gly Ile Pro Gly Glu Lys Gly Lys Ala Gly Thr Val Cys Asp
 110 115 120
 Cys Gly Arg Tyr Arg Lys Phe Val Gly Gln Leu Asp Ile Ser Ile
 125 130 135
 Ala Arg Leu Lys Thr Ser Met Lys Phe Val Lys Asn Val Ile Ala
 140 145 150
 Gly Ile Arg Glu Thr Glu Glu Lys Phe Tyr Tyr Ile Val Gln Glu
 155 160 165
 Glu Lys Asn Tyr Arg Glu Ser Leu Thr His Cys Arg Ile Arg Gly
 170 175 180
 Gly Met Leu Ala Met Pro Lys Asp Glu Ala Ala Asn Thr Leu Ile
 185 190 195
 Ala Asp Tyr Val Ala Lys Ser Gly Phe Phe Arg Val Phe Ile Gly

200	205	210
Val Asn Asp Leu Glu Arg Glu Gly Gln Tyr Met Ser Thr Asp Asn		
215	220	225
Thr Pro Leu Gln Asn Tyr Ser Asn Trp Asn Glu Gly Glu Pro Ser		
230	235	240
Asp Pro Tyr Gly His Glu Asp Cys Val Glu Met Leu Ser Ser Gly		
245	250	255
Arg Trp Asn Asp Thr Glu Cys His Leu Thr Met Tyr Phe Val Cys		
260	265	270
Glu Phe Ile Lys Lys Lys Lys		
275		

<210> 98

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 98

cgctgactat gttgccaaga gtgg 24

<210> 99

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 99

gatgatggag gctccatacc tcag 24

<210> 100

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 100

gtgttcattg gcgtgaatga ccttgaaagg gagggacagt acatgttcac 50

<210> 101

<211> 2574

<212> DNA

<213> Homo sapiens

<400> 101

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gagaagtctc agctagaacg agcggcccta ggttttcgga agggaggatc 200
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catggcccaa cttgtttatt gcag 2574

<210> 102

<211> 730

<212> PRT

<213> Homo sapiens

<400> 102

Met	Gly	Val	Cys	Gln	Arg	Thr	Arg	Ala	Pro	Trp	Lys	Glu	Lys	Ser
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Gln	Leu	Glu	Arg	Ala	Ala	Leu	Gly	Phe	Arg	Lys	Gly	Gly	Ser	Gly
				20					25					30

Met	Phe	Ala	Ser	Gly	Trp	Asn	Gln	Thr	Val	Pro	Ile	Glu	Glu	Ala	35	40	45
Gly	Ser	Met	Ala	Ala	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	50	55	60
Pro	Leu	Leu	Leu	Leu	Lys	Leu	His	Leu	Trp	Pro	Gln	Leu	Arg	Trp	65	70	75
Leu	Pro	Ala	Asp	Leu	Ala	Phe	Ala	Val	Arg	Ala	Leu	Cys	Cys	Lys	80	85	90
Arg	Ala	Leu	Arg	Ala	Arg	Ala	Leu	Ala	Ala	Ala	Ala	Ala	Asp	Pro	95	100	105
Glu	Gly	Pro	Glu	Gly	Gly	Cys	Ser	Leu	Ala	Trp	Arg	Leu	Ala	Glu	110	115	120
Leu	Ala	Gln	Gln	Arg	Ala	Ala	His	Thr	Phe	Leu	Ile	His	Gly	Ser	125	130	135
Arg	Arg	Phe	Ser	Tyr	Ser	Glu	Ala	Glu	Arg	Glu	Ser	Asn	Arg	Ala	140	145	150
Ala	Arg	Ala	Phe	Leu	Arg	Ala	Leu	Gly	Trp	Asp	Trp	Gly	Pro	Asp	155	160	165
Gly	Gly	Asp	Ser	Gly	Glu	Gly	Ser	Ala	Gly	Glu	Gly	Glu	Arg	Ala	170	175	180
Ala	Pro	Gly	Ala	Gly	Asp	Ala	Ala	Ala	Gly	Ser	Gly	Ala	Glu	Phe	185	190	195
Ala	Gly	Gly	Asp	Gly	Ala	Ala	Arg	Gly	Gly	Gly	Ala	Ala	Ala	Pro	200	205	210
Leu	Ser	Pro	Gly	Ala	Thr	Val	Ala	Leu	Leu	Leu	Pro	Ala	Gly	Pro	215	220	225
Glu	Phe	Leu	Trp	Leu	Trp	Phe	Gly	Leu	Ala	Lys	Ala	Gly	Leu	Arg	230	235	240
Thr	Ala	Phe	Val	Pro	Thr	Ala	Leu	Arg	Arg	Gly	Pro	Leu	Leu	His	245	250	255
Cys	Leu	Arg	Ser	Cys	Gly	Ala	Arg	Ala	Leu	Val	Leu	Ala	Pro	Glu	260	265	270
Phe	Leu	Glu	Ser	Leu	Glu	Pro	Asp	Leu	Pro	Ala	Leu	Arg	Ala	Met	275	280	285
Gly	Leu	His	Leu	Trp	Ala	Ala	Gly	Pro	Gly	Thr	His	Pro	Ala	Gly	290	295	300
Ile	Ser	Asp	Leu	Leu	Ala	Glu	Val	Ser	Ala	Glu	Val	Asp	Gly	Pro	305	310	315

Val Pro Gly Tyr	Leu Ser Ser Pro Gln	Ser Ile Thr Asp Thr	Cys
320	325		330
Leu Tyr Ile Phe	Thr Ser Gly Thr Thr	Gly Leu Pro Lys Ala	Ala
335	340		345
Arg Ile Ser His	Leu Lys Ile Leu Gln	Cys Gln Gly Phe Tyr	Gln
350	355		360
Leu Cys Gly Val	His Gln Glu Asp Val	Ile Tyr Leu Ala Leu	Pro
365	370		375
Leu Tyr His Met	Ser Gly Ser Leu Leu	Gly Ile Val Gly Cys	Met
380	385		390
Gly Ile Gly Ala	Thr Val Val Leu Lys	Ser Lys Phe Ser Ala	Gly
395	400		405
Gln Phe Trp Glu	Asp Cys Gln Gln His	Arg Val Thr Val Phe	Gln
410	415		420
Tyr Ile Gly Glu	Leu Cys Arg Tyr Leu	Val Asn Gln Pro Pro	Ser
425	430		435
Lys Ala Glu Arg	Gly His Lys Val Arg	Leu Ala Val Gly Ser	Gly
440	445		450
Leu Arg Pro Asp	Thr Trp Glu Arg Phe	Val Arg Arg Phe Gly	Pro
455	460		465
Leu Gln Val Leu	Glu Thr Tyr Gly Leu	Thr Glu Gly Asn Val	Ala
470	475		480
Thr Ile Asn Tyr	Thr Gly Gln Arg Gly	Ala Val Gly Arg Ala	Ser
485	490		495
Trp Leu Tyr Lys	His Ile Phe Pro Phe	Ser Leu Ile Arg Tyr	Asp
500	505		510
Val Thr Thr Gly	Glu Pro Ile Arg Asp	Pro Gln Gly His Cys	Met
515	520		525
Ala Thr Ser Pro	Gly Glu Pro Gly Leu	Leu Val Ala Pro Val	Ser
530	535		540
Gln Gln Ser Pro	Phe Leu Gly Tyr Ala	Gly Gly Pro Glu Leu	Ala
545	550		555
Gln Gly Lys Leu	Leu Lys Asp Val Phe	Arg Pro Gly Asp Val	Phe
560	565		570
Phe Asn Thr Gly	Asp Leu Leu Val Cys	Asp Asp Gln Gly Phe	Leu
575	580		585
Arg Phe His Asp	Arg Thr Gly Asp Thr	Phe Arg Trp Lys Gly	Glu
590	595		600

Asn	Val	Ala	Thr	Thr	Glu	Val	Ala	Glu	Val	Phe	Glu	Ala	Leu	Asp
				605					610					615
Phe	Leu	Gln	Glu	Val	Asn	Val	Tyr	Gly	Val	Thr	Val	Pro	Gly	His
				620					625					630
Glu	Gly	Arg	Ala	Gly	Met	Ala	Ala	Leu	Val	Leu	Arg	Pro	Pro	His
				635					640					645
Ala	Leu	Asp	Leu	Met	Gln	Leu	Tyr	Thr	His	Val	Ser	Glu	Asn	Leu
				650					655					660
Pro	Pro	Tyr	Ala	Arg	Pro	Arg	Phe	Leu	Arg	Leu	Gln	Glu	Ser	Leu
				665					670					675
Ala	Thr	Thr	Glu	Thr	Phe	Lys	Gln	Gln	Lys	Val	Arg	Met	Ala	Asn
				680					685					690
Glu	Gly	Phe	Asp	Pro	Ser	Thr	Leu	Ser	Asp	Pro	Leu	Tyr	Val	Leu
				695					700					705
Asp	Gln	Ala	Val	Gly	Ala	Tyr	Leu	Pro	Leu	Thr	Thr	Ala	Arg	Tyr
				710					715					720
Ser	Ala	Leu	Leu	Ala	Gly	Asn	Leu	Arg	Ile					
				725					730					

<210> 103

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 103

gagagccatg gggctccacc tg 22

<210> 104

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 104

ggagaatgtg gccacaac 18

<210> 105

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 105

gccctggcac agtgactcca tagacg 26

<210> 106

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 106

atccacttca gcggacac 18

<210> 107

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 107

ccagtgccag gatacctctc ttccccccag agcataacag acacg 45

<210> 108

<211> 2579

<212> DNA

<213> Homo sapiens

<400> 108

cctgtgttaa gctgagggtt cccctagatc tcgtatatcc ccaacacata 50

cctccacgca cacacatccc caagaacctc gagctcacac caacagacac 100

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ccggcgcgcg ctcccacctt tgccgcacac tccggcgagc cgagccccga 200

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<210> 109

<211> 555

<212> PRT

<213> Homo sapiens

<400> 109

Met	Pro	Ser	Trp	Ile	Gly	Ala	Val	Ile	Leu	Pro	Leu	Leu	Gly	Leu	1	5	10	15
Leu	Leu	Ser	Leu	Pro	Ala	Gly	Ala	Asp	Val	Lys	Ala	Arg	Ser	Cys	20	25	30	
Gly	Glu	Val	Arg	Gln	Ala	Tyr	Gly	Ala	Lys	Gly	Phe	Ser	Leu	Ala	35	40	45	
Asp	Ile	Pro	Tyr	Gln	Glu	Ile	Ala	Gly	Glu	His	Leu	Arg	Ile	Cys	50	55	60	
Pro	Gln	Glu	Tyr	Thr	Cys	Cys	Thr	Thr	Glu	Met	Glu	Asp	Lys	Leu	65	70	75	
Ser	Gln	Gln	Ser	Lys	Leu	Glu	Phe	Glu	Asn	Leu	Val	Glu	Glu	Thr	80	85	90	
Ser	His	Phe	Val	Arg	Thr	Thr	Phe	Val	Ser	Arg	His	Lys	Lys	Phe	95	100	105	
Asp	Glu	Phe	Phe	Arg	Glu	Leu	Leu	Glu	Asn	Ala	Glu	Lys	Ser	Leu	110	115	120	
Asn	Asp	Met	Phe	Val	Arg	Thr	Tyr	Gly	Met	Leu	Tyr	Met	Gln	Asn	125	130	135	
Ser	Glu	Val	Phe	Gln	Asp	Leu	Phe	Thr	Glu	Leu	Lys	Arg	Tyr	Tyr	140	145	150	

Thr Gly Gly Asn Val Asn Leu Glu Glu Met Leu Asn Asp Phe Trp	155	160	165
Ala Arg Leu Leu Glu Arg Met Phe Gln Leu Ile Asn Pro Gln Tyr	170	175	180
His Phe Ser Glu Asp Tyr Leu Glu Cys Val Ser Lys Tyr Thr Asp	185	190	195
Gln Leu Lys Pro Phe Gly Asp Val Pro Arg Lys Leu Lys Ile Gln	200	205	210
Val Thr Arg Ala Phe Ile Ala Ala Arg Thr Phe Val Gln Gly Leu	215	220	225
Thr Val Gly Arg Glu Val Ala Asn Arg Val Ser Lys Val Ser Pro	230	235	240
Thr Pro Gly Cys Ile Arg Ala Leu Met Lys Met Leu Tyr Cys Pro	245	250	255
Tyr Cys Arg Gly Leu Pro Thr Val Arg Pro Cys Asn Asn Tyr Cys	260	265	270
Leu Asn Val Met Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp	275	280	285
Thr Glu Trp Asn Leu Phe Ile Asp Ala Met Leu Leu Val Ala Glu	290	295	300
Arg Leu Glu Gly Pro Phe Asn Ile Glu Ser Val Met Asp Pro Ile	305	310	315
Asp Val Lys Ile Ser Glu Ala Ile Met Asn Met Gln Glu Asn Ser	320	325	330
Met Gln Val Ser Ala Lys Val Phe Gln Gly Cys Gly Gln Pro Lys	335	340	345
Pro Ala Pro Ala Leu Arg Ser Ala Arg Ser Ala Pro Glu Asn Phe	350	355	360
Asn Thr Arg Phe Arg Pro Tyr Asn Pro Glu Glu Arg Pro Thr Thr	365	370	375
Ala Ala Gly Thr Ser Leu Asp Arg Leu Val Thr Asp Ile Lys Glu	380	385	390
Lys Leu Lys Leu Ser Lys Lys Val Trp Ser Ala Leu Pro Tyr Thr	395	400	405
Ile Cys Lys Asp Glu Ser Val Thr Ala Gly Thr Ser Asn Glu Glu	410	415	420
Glu Cys Trp Asn Gly His Ser Lys Ala Arg Tyr Leu Pro Glu Ile	425	430	435

Met	Asn	Asp	Gly	Leu	Thr	Asn	Gln	Ile	Asn	Asn	Pro	Glu	Val	Asp
				440					445					450
Val	Asp	Ile	Thr	Arg	Pro	Asp	Thr	Phe	Ile	Arg	Gln	Gln	Ile	Met
				455					460					465
Ala	Leu	Arg	Val	Met	Thr	Asn	Lys	Leu	Lys	Asn	Ala	Tyr	Asn	Gly
				470					475					480
Asn	Asp	Val	Asn	Phe	Gln	Asp	Thr	Ser	Asp	Glu	Ser	Ser	Gly	Ser
				485					490					495
Gly	Ser	Gly	Ser	Gly	Cys	Met	Asp	Asp	Val	Cys	Pro	Thr	Glu	Phe
				500					505					510
Glu	Phe	Val	Thr	Thr	Glu	Ala	Pro	Ala	Val	Asp	Pro	Asp	Arg	Arg
				515					520					525
Glu	Val	Asp	Ser	Ser	Ala	Ala	Gln	Arg	Gly	His	Ser	Leu	Leu	Ser
				530					535					540
Trp	Ser	Leu	Thr	Cys	Ile	Val	Leu	Ala	Leu	Gln	Arg	Leu	Cys	Arg
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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 111

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<212> DNA

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<223> Synthetic oligonucleotide probe

<400> 112

gaatgctgga acgggcacag caaagccaga tacttgctg 40

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<213> Homo sapiens

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<211> 515

<212> PRT

<213> Homo sapiens

<400> 114

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Ala	Gly	Phe	Trp	Ile	Leu	Cys	Leu	Leu	Thr	Tyr	Gly	Tyr	Leu	Ser	35	40	45	
Trp	Gly	Gln	Ala	Leu	Glu	Glu	Glu	Glu	Glu	Gly	Ala	Leu	Leu	Ala	50	55	60	
Gln	Ala	Gly	Glu	Lys	Leu	Glu	Pro	Ser	Thr	Thr	Ser	Thr	Ser	Gln	65	70	75	
Pro	His	Leu	Ile	Phe	Ile	Leu	Ala	Asp	Asp	Gln	Gly	Phe	Arg	Asp	80	85	90	
Val	Gly	Tyr	His	Gly	Ser	Glu	Ile	Lys	Thr	Pro	Thr	Leu	Asp	Lys	95	100	105	
Leu	Ala	Ala	Glu	Gly	Val	Lys	Leu	Glu	Asn	Tyr	Tyr	Val	Gln	Pro	110	115	120	
Ile	Cys	Thr	Pro	Ser	Arg	Ser	Gln	Phe	Ile	Thr	Gly	Lys	Tyr	Gln	125	130	135	
Ile	His	Thr	Gly	Leu	Gln	His	Ser	Ile	Ile	Arg	Pro	Thr	Gln	Pro	140	145	150	

Asn	Cys	Leu	Pro	Leu	Asp	Asn	Ala	Thr	Leu	Pro	Gln	Lys	Leu	Lys		155	160	165
Glu	Val	Gly	Tyr	Ser	Thr	His	Met	Val	Gly	Lys	Trp	His	Leu	Gly		170	175	180
Phe	Asn	Arg	Lys	Glu	Cys	Met	Pro	Thr	Arg	Arg	Gly	Phe	Asp	Thr		185	190	195
Phe	Phe	Gly	Ser	Leu	Leu	Gly	Ser	Gly	Asp	Tyr	Tyr	Thr	His	Tyr		200	205	210
Lys	Cys	Asp	Ser	Pro	Gly	Met	Cys	Gly	Tyr	Asp	Leu	Tyr	Glu	Asn		215	220	225
Asp	Asn	Ala	Ala	Trp	Asp	Tyr	Asp	Asn	Gly	Ile	Tyr	Ser	Thr	Gln		230	235	240
Met	Tyr	Thr	Gln	Arg	Val	Gln	Gln	Ile	Leu	Ala	Ser	His	Asn	Pro		245	250	255
Thr	Lys	Pro	Ile	Phe	Leu	Tyr	Thr	Ala	Tyr	Gln	Ala	Val	His	Ser		260	265	270
Pro	Leu	Gln	Ala	Pro	Gly	Arg	Tyr	Phe	Glu	His	Tyr	Arg	Ser	Ile		275	280	285
Ile	Asn	Ile	Asn	Arg	Arg	Arg	Tyr	Ala	Ala	Met	Leu	Ser	Cys	Leu		290	295	300
Asp	Glu	Ala	Ile	Asn	Asn	Val	Thr	Leu	Ala	Leu	Lys	Thr	Tyr	Gly		305	310	315
Phe	Tyr	Asn	Asn	Ser	Ile	Ile	Ile	Tyr	Ser	Ser	Asp	Asn	Gly	Gly		320	325	330
Gln	Pro	Thr	Ala	Gly	Gly	Ser	Asn	Trp	Pro	Leu	Arg	Gly	Ser	Lys		335	340	345
Gly	Thr	Tyr	Trp	Glu	Gly	Gly	Ile	Arg	Ala	Val	Gly	Phe	Val	His		350	355	360
Ser	Pro	Leu	Leu	Lys	Asn	Lys	Gly	Thr	Val	Cys	Lys	Glu	Leu	Val		365	370	375
His	Ile	Thr	Asp	Trp	Tyr	Pro	Thr	Leu	Ile	Ser	Leu	Ala	Glu	Gly		380	385	390
Gln	Ile	Asp	Glu	Asp	Ile	Gln	Leu	Asp	Gly	Tyr	Asp	Ile	Trp	Glu		395	400	405
Thr	Ile	Ser	Glu	Gly	Leu	Arg	Ser	Pro	Arg	Val	Asp	Ile	Leu	His		410	415	420
Asn	Ile	Asp	Pro	Tyr	Thr	Pro	Arg	Gln	Lys	Met	Ala	Pro	Gly	Gln		425	430	435

Gln Ala Met Gly Ser Gly Thr Leu Gln Ser Ser Gln Pro Ser Glu
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Cys Ser Thr Gly Asn Cys Leu Gln Glu Ile Leu Ala Thr Ala Thr
455 460 465

Gly Ser Pro Leu Ser Leu Ser Ala Thr Trp Asp Arg Thr Gly Gly
470 475 480

Thr Met Asn Gly Ser Pro Cys Gln Leu Ala Lys Val Tyr Gly Phe
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Gly Ile Gln Glu Ser
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 115

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<210> 116

<211> 24

<212> DNA

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<220>

<223> Synthetic oligonucleotide probe

<400> 116

ctctctgagt gtacatctgt gtgg 24

<210> 117

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<220>

<221> unsure

<222> 33

<223> unknown base

<400> 117

gccaccctac ctcagaaact gaaggagggtt ggntattcaa cgcatatggt 50

cgg 53

<210> 118

<211> 2260

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2009, 2026, 2033, 2055, 2074, 2078, 2086

<223> unknown base

<400> 118

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<210> 119

<211> 338

<212> PRT

<213> Homo sapiens

<400> 119

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Val	Ala	Gly	Gly	Phe	Gly	Asn	Ala	Ala	Ser	Ala	Arg	His	His	Gly		20	25	30
Leu	Leu	Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr		35	40	45
Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val		50	55	60
Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val		65	70	75
Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr		80	85	90
Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys		95	100	105
Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys		110	115	120
Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser		125	130	135
Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr		140	145	150
Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu		155	160	165
Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser		170	175	180
Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe		185	190	195
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr		200	205	210
Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met		215	220	225
Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln		230	235	240
Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly		245	250	255
Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu		260	265	270
Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala		275	280	285
His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr		290	295	300

Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro
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Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly
320 325 330

Gly Lys Lys Gly Asn Glu Glu Lys
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<210> 120

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 120

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 122

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 122

gataaactgt cagtacagct gtgaagacac agaagaaggg ccacagtgcc 50

<210> 123

<211> 1199

<212> DNA

<213> Homo sapiens

<400> 123

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aatggaaaac atgaaaacag caatcttctt atgcttctga ataataaag 1100
actaatttgt gattttactt tttaatagat atgactttgc ttccaacatg 1150
gaatgaaata aaaaataaat aataaaagat tgccatgaat cttgcaaaa 1199

<210> 124

<211> 289

<212> PRT

<213> Homo sapiens

<400> 124

Met	Val	Val	Trp	Val	Thr	Gly	Ala	Ser	Ser	Gly	Ile	Gly	Glu	Glu
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Leu	Ala	Tyr	Gln	Leu	Ser	Lys	Leu	Gly	Val	Ser	Leu	Val	Leu	Ser
			20					25					30	
Ala	Arg	Arg	Val	His	Glu	Leu	Glu	Arg	Val	Lys	Arg	Arg	Cys	Leu
			35					40					45	
Glu	Asn	Gly	Asn	Leu	Lys	Glu	Lys	Asp	Ile	Leu	Val	Leu	Pro	Leu
			50					55					60	

Asp	Leu	Thr	Asp	Thr	Gly	Ser	His	Glu	Ala	Ala	Thr	Lys	Ala	Val	65	70	75
Leu	Gln	Glu	Phe	Gly	Arg	Ile	Asp	Ile	Leu	Val	Asn	Asn	Gly	Gly	80	85	90
Met	Ser	Gln	Arg	Ser	Leu	Cys	Met	Asp	Thr	Ser	Leu	Asp	Val	Tyr	95	100	105
Arg	Lys	Leu	Ile	Glu	Leu	Asn	Tyr	Leu	Gly	Thr	Val	Ser	Leu	Thr	110	115	120
Lys	Cys	Val	Leu	Pro	His	Met	Ile	Glu	Arg	Lys	Gln	Gly	Lys	Ile	125	130	135
Val	Thr	Val	Asn	Ser	Ile	Leu	Gly	Ile	Ile	Ser	Val	Pro	Leu	Ser	140	145	150
Ile	Gly	Tyr	Cys	Ala	Ser	Lys	His	Ala	Leu	Arg	Gly	Phe	Phe	Asn	155	160	165
Gly	Leu	Arg	Thr	Glu	Leu	Ala	Thr	Tyr	Pro	Gly	Ile	Ile	Val	Ser	170	175	180
Asn	Ile	Cys	Pro	Gly	Pro	Val	Gln	Ser	Asn	Ile	Val	Glu	Asn	Ser	185	190	195
Leu	Ala	Gly	Glu	Val	Thr	Lys	Thr	Ile	Gly	Asn	Asn	Gly	Asp	Gln	200	205	210
Ser	His	Lys	Met	Thr	Thr	Ser	Arg	Cys	Val	Arg	Leu	Met	Leu	Ile	215	220	225
Ser	Met	Ala	Asn	Asp	Leu	Lys	Glu	Val	Trp	Ile	Ser	Glu	Gln	Pro	230	235	240
Phe	Leu	Leu	Val	Thr	Tyr	Leu	Trp	Gln	Tyr	Met	Pro	Thr	Trp	Ala	245	250	255
Trp	Trp	Ile	Thr	Asn	Lys	Met	Gly	Lys	Lys	Arg	Ile	Glu	Asn	Phe	260	265	270
Lys	Ser	Gly	Val	Asp	Ala	Asp	Ser	Ser	Tyr	Phe	Lys	Ile	Phe	Lys	275	280	285

Thr Lys His Asp

<210> 125

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 125

gcaatgaact gggagctgc 19

<210> 126

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

ctgtgaatag catcctggg 19

<210> 127

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 127

cttttcaagc cactggagg 20

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 128

ctgtagacat ccaagctggt atcc 24

<210> 129

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 129

aagagtctgc atccacacca ctc 23

<210> 130

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 130

acctgacgct actatgggcc gagtggcagg gacgacgcc agaag 46

<210> 131
<211> 2365
<212> DNA
<213> Homo sapiens

<400> 131
gcgacgtggg caccgccatc agctgttcgc gcgtcttctc ctccaggtgg 50
ggcaggggtt tcgggctggt ggagcatgtg ctgggacagg acagcatcct 100
caatcaatcc aacagcatat tcggttgcat cttctacaca ctacagctat 150
tgtaggttg cctgcggaca cgctgggcct ctgtcctgat gctgctgagc 200
tccctggtgt ctctcgctgg ttctgtctac ctggcctgga tcctgttctt 250
cgtgctctat gatttctgca ttgtttgtat caccacctat gctatcaacg 300
tgagcctgat gtggctcagt ttccggaagg tccaagaacc ccagggcaag 350
gctaagaggc actgagccct caaccaagc caggctgacc tcattctgctt 400
tgctttggtc ttcaagccgc tcagcgtgcc tgtggacagc gtggccccgg 450
ccccccaag cctcaggagg gcaacacagt ccctggcgag tggccctggc 500
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<210> 132
 <211> 571
 <212> PRT
 <213> Homo sapiens

<400> 132
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 Ala Trp Ile Leu Phe Phe Val Leu Tyr Asp Phe Cys Ile Val Cys
 20 25 30

Ile Thr Thr Tyr Ala	Ile Asn Val Ser Leu Met Trp Leu Ser Phe	35	40	45
Arg Lys Val Gln Glu	Pro Gln Gly Lys Ala Lys Arg His Gly Asn	50	55	60
Thr Val Pro Gly Glu	Trp Pro Trp Gln Ala Ser Val Arg Arg Gln	65	70	75
Gly Ala His Ile Cys	Ser Gly Ser Leu Val Ala Asp Thr Trp Val	80	85	90
Leu Thr Ala Ala His	Cys Phe Glu Lys Ala Ala Ala Thr Glu Leu	95	100	105
Asn Ser Trp Ser Val	Val Leu Gly Ser Leu Gln Arg Glu Gly Leu	110	115	120
Ser Pro Gly Ala Glu	Glu Val Gly Val Ala Ala Leu Gln Leu Pro	125	130	135
Arg Ala Tyr Asn His	Tyr Ser Gln Gly Ser Asp Leu Ala Leu Leu	140	145	150
Gln Leu Ala His Pro	Thr Thr His Thr Pro Leu Cys Leu Pro Gln	155	160	165
Pro Ala His Arg Phe	Pro Phe Gly Ala Ser Cys Trp Ala Thr Gly	170	175	180
Trp Asp Gln Asp Thr	Ser Asp Ala Pro Gly Thr Leu Arg Asn Leu	185	190	195
Arg Leu Arg Leu Ile	Ser Arg Pro Thr Cys Asn Cys Ile Tyr Asn	200	205	210
Gln Leu His Gln Arg	His Leu Ser Asn Pro Ala Arg Pro Gly Met	215	220	225
Leu Cys Gly Gly Pro	Gln Pro Gly Val Gln Gly Pro Cys Gln Gly	230	235	240
Asp Ser Gly Gly Pro	Val Leu Cys Leu Glu Pro Asp Gly His Trp	245	250	255
Val Gln Ala Gly Ile	Ile Ser Phe Ala Ser Ser Cys Ala Gln Glu	260	265	270
Asp Ala Pro Val Leu	Leu Thr Asn Thr Ala Ala His Ser Ser Trp	275	280	285
Leu Gln Ala Arg Val	Gln Gly Ala Ala Phe Leu Ala Gln Ser Pro	290	295	300
Glu Thr Pro Glu Met	Ser Asp Glu Asp Ser Cys Val Ala Cys Gly	305	310	315

Ser	Leu	Arg	Thr	Ala	Gly	Pro	Gln	Ala	Gly	Ala	Pro	Ser	Pro	Trp	320	325	330
Pro	Trp	Glu	Ala	Arg	Leu	Met	His	Gln	Gly	Gln	Leu	Ala	Cys	Gly	335	340	345
Gly	Ala	Leu	Val	Ser	Glu	Glu	Ala	Val	Leu	Thr	Ala	Ala	His	Cys	350	355	360
Phe	Ile	Gly	Arg	Gln	Ala	Pro	Glu	Glu	Trp	Ser	Val	Gly	Leu	Gly	365	370	375
Thr	Arg	Pro	Glu	Glu	Trp	Gly	Leu	Lys	Gln	Leu	Ile	Leu	His	Gly	380	385	390
Ala	Tyr	Thr	His	Pro	Glu	Gly	Gly	Tyr	Asp	Met	Ala	Leu	Leu	Leu	395	400	405
Leu	Ala	Gln	Pro	Val	Thr	Leu	Gly	Ala	Ser	Leu	Arg	Pro	Leu	Cys	410	415	420
Leu	Pro	Tyr	Pro	Asp	His	His	Leu	Pro	Asp	Gly	Glu	Arg	Gly	Trp	425	430	435
Val	Leu	Gly	Arg	Ala	Arg	Pro	Gly	Ala	Gly	Ile	Ser	Ser	Leu	Gln	440	445	450
Thr	Val	Pro	Val	Thr	Leu	Leu	Gly	Pro	Arg	Ala	Cys	Ser	Arg	Leu	455	460	465
His	Ala	Ala	Pro	Gly	Gly	Asp	Gly	Ser	Pro	Ile	Leu	Pro	Gly	Met	470	475	480
Val	Cys	Thr	Ser	Ala	Val	Gly	Glu	Leu	Pro	Ser	Cys	Glu	Gly	Leu	485	490	495
Ser	Gly	Ala	Pro	Leu	Val	His	Glu	Val	Arg	Gly	Thr	Trp	Phe	Leu	500	505	510
Ala	Gly	Leu	His	Ser	Phe	Gly	Asp	Ala	Cys	Gln	Gly	Pro	Ala	Arg	515	520	525
Pro	Ala	Val	Phe	Thr	Ala	Leu	Pro	Ala	Tyr	Glu	Asp	Trp	Val	Ser	530	535	540
Ser	Leu	Asp	Trp	Gln	Val	Tyr	Phe	Ala	Glu	Glu	Pro	Glu	Pro	Glu	545	550	555
Ala	Glu	Pro	Gly	Ser	Cys	Leu	Ala	Asn	Ile	Ser	Gln	Pro	Thr	Ser	560	565	570

Cys

<210> 133

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 133

cctgtgctgt gcctcgagcc tgac 24

<210> 134

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134

gtgggcagca gttagcaccg cctc 24

<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 135

ggctggcatc atcagctttg catcaagctg tgcccaggag gacgc 45

<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 136

cgggccgccc ccggccccca ttcgggccgg gcctcgctgc ggcgcgact 50

gagccaggct gggccgcgtc cctgagtcct agagtcggcg cggcgcgga 100

ggggcagcct tccaccacgg ggagcccagc tgtcagccgc ctcacaggaa 150

gatgctgcgt cggcggggca gccctggcat ggggtgtcat gtgggtgcag 200

ccctgggagc actgtggttc tgcctcacag gagccctgga ggtccaggtc 250

cctgaagacc cagtgtgtggc actggtgggc accgatgcca ccctgtgctg 300

ctccttctcc cctgagcctg gcttcagcct ggcacagctc aacctcatct 350

ggcagctgac agatacaaaa cagctggtgc acagctttgc tgagggccag 400

gaccagggca ggcctatgc caaccgcacg gccctcttcc cggacctgct 450

ggcacagggc aacgcatccc tgaggctgca gcgcgtgcgt gtggcggaag 500

agggcagctt cacctgcttc gtgagcatcc gggatttcgg cagcgctgcc 550

gtcagcctgc aggtggccgc tccctactcg aagcccagca tgaccctgga 600
gccaacaag gacctgcggc caggggacac ggtgaccatc acgtgctcca 650
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atgccttccg gatgtcatct ctccctgccc caggaatgga agatgtgagg 1900
acttctaatt taaatgtggg actcggaggg attttgtaa ctgggggtat 1950

attttgggga aaataaatgt ctttgtaaaa aaaaaaaaaa aaaaaaaaa 1998

<210> 137

<211> 316

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 233

<223> unknown amino acid

<400> 137

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				20					25					30	
Val	Gln	Val	Pro	Glu	Asp	Pro	Val	Val	Ala	Leu	Val	Gly	Thr	Asp	
				35					40					45	
Ala	Thr	Leu	Cys	Cys	Ser	Phe	Ser	Pro	Glu	Pro	Gly	Phe	Ser	Leu	
				50					55					60	
Ala	Gln	Leu	Asn	Leu	Ile	Trp	Gln	Leu	Thr	Asp	Thr	Lys	Gln	Leu	
				65					70					75	
Val	His	Ser	Phe	Ala	Glu	Gly	Gln	Asp	Gln	Gly	Ser	Ala	Tyr	Ala	
				80					85					90	
Asn	Arg	Thr	Ala	Leu	Phe	Pro	Asp	Leu	Leu	Ala	Gln	Gly	Asn	Ala	
				95					100					105	
Ser	Leu	Arg	Leu	Gln	Arg	Val	Arg	Val	Ala	Asp	Glu	Gly	Ser	Phe	
				110					115					120	
Thr	Cys	Phe	Val	Ser	Ile	Arg	Asp	Phe	Gly	Ser	Ala	Ala	Val	Ser	
				125					130					135	
Leu	Gln	Val	Ala	Ala	Pro	Tyr	Ser	Lys	Pro	Ser	Met	Thr	Leu	Glu	
				140					145					150	
Pro	Asn	Lys	Asp	Leu	Arg	Pro	Gly	Asp	Thr	Val	Thr	Ile	Thr	Cys	
				155					160					165	
Ser	Ser	Tyr	Gln	Gly	Tyr	Pro	Glu	Ala	Glu	Val	Phe	Trp	Gln	Asp	
				170					175					180	
Gly	Gln	Gly	Val	Pro	Leu	Thr	Gly	Asn	Val	Thr	Thr	Ser	Gln	Met	
				185					190					195	
Ala	Asn	Glu	Gln	Gly	Leu	Phe	Asp	Val	His	Ser	Val	Leu	Arg	Val	
				200					205					210	
Val	Leu	Gly	Ala	Asn	Gly	Thr	Tyr	Ser	Cys	Leu	Val	Arg	Asn	Pro	
				215					220					225	

Val	Leu	Gln	Gln	Asp	Ala	His	Xaa	Ser	Val	Thr	Ile	Thr	Gly	Gln
				230					235					240
Pro	Met	Thr	Phe	Pro	Pro	Glu	Ala	Leu	Trp	Val	Thr	Val	Gly	Leu
				245					250					255
Ser	Val	Cys	Leu	Ile	Ala	Leu	Leu	Val	Ala	Leu	Ala	Phe	Val	Cys
				260					265					270
Trp	Arg	Lys	Ile	Lys	Gln	Ser	Cys	Glu	Glu	Glu	Asn	Ala	Gly	Ala
				275					280					285
Glu	Asp	Gln	Asp	Gly	Glu	Gly	Glu	Gly	Ser	Lys	Thr	Ala	Leu	Gln
				290					295					300
Pro	Leu	Lys	His	Ser	Asp	Ser	Lys	Glu	Asp	Asp	Gly	Gln	Glu	Ile
				305					310					315

Ala

<210> 138

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 138

ctggcacagc tcaacctcat ctgg 24

<210> 139

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 139

gctgtctgtc tgtctcattg 20

<210> 140

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 140

ggacacagta tactgaccac 20

<210> 141

<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 141
tgccaaccag gcagctgtaa gtgc 24

<210> 142
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 142
tggaagaaga ggggtggtgat gtgg 24

<210> 143
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 143
cagctgacag acaccaaaca gctggtgcac agtttcaccg aaggc 45

<210> 144
<211> 2336
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1620, 1673
<223> unknown base

<400> 144
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tacgttctta aatctatgaa gtcgaggac ctttcgctgc ttttgtaggg 150
acttctttcc ttgcttcagc aacatgaggc ttttcttggtg gaacgcggtc 200
ttgactctgt tcgtcacttc tttgattggg gctttgatcc ctgaaccaga 250
agtgaaaatt gaagttctcc agaagccatt catctgccat cgcaagacca 300
aaggagggga tttgatgttg gtccactatg aaggctactt agaaaaggac 350
ggctccttat ttcactccac tcacaaacat aacaatggtc agcccatttg 400

gtttaccctg ggcacccctg aggcctctcaa aggttgggac cagggccttga 450
aaggaatgtg ttaggagag aagagaaagc tcatcattcc tcctgctctg 500
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cattccaaga aatggatctt aatgatgact ggaaactctc taaagatgag 650
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aagacaaaga tgggtttata tctgccagag aatttacata taaacacgat 800
gagttataga gatacatcta cccttttaac atagcactca tctttcaaga 850
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<210> 145

<211> 211

<212> PRT

<213> Homo sapiens

<400> 145

Met	Arg	Leu	Phe	Leu	Trp	Asn	Ala	Val	Leu	Thr	Leu	Phe	Val	Thr
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Ser	Leu	Ile	Gly	Ala	Leu	Ile	Pro	Glu	Pro	Glu	Val	Lys	Ile	Glu
			20					25						30
Val	Leu	Gln	Lys	Pro	Phe	Ile	Cys	His	Arg	Lys	Thr	Lys	Gly	Gly
			35					40						45
Asp	Leu	Met	Leu	Val	His	Tyr	Glu	Gly	Tyr	Leu	Glu	Lys	Asp	Gly
			50					55						60
Ser	Leu	Phe	His	Ser	Thr	His	Lys	His	Asn	Asn	Gly	Gln	Pro	Ile
			65					70						75
Trp	Phe	Thr	Leu	Gly	Ile	Leu	Glu	Ala	Leu	Lys	Gly	Trp	Asp	Gln
			80					85						90
Gly	Leu	Lys	Gly	Met	Cys	Val	Gly	Glu	Lys	Arg	Lys	Leu	Ile	Ile
			95					100						105
Pro	Pro	Ala	Leu	Gly	Tyr	Gly	Lys	Glu	Gly	Lys	Gly	Lys	Ile	Pro
			110					115						120
Pro	Glu	Ser	Thr	Leu	Ile	Phe	Asn	Ile	Asp	Leu	Leu	Glu	Ile	Arg
			125					130						135
Asn	Gly	Pro	Arg	Ser	His	Glu	Ser	Phe	Gln	Glu	Met	Asp	Leu	Asn
			140					145						150

Asp Asp Trp Lys Leu Ser Lys Asp Glu Val Lys Ala Tyr Leu Lys
155 160 165

Lys Glu Phe Glu Lys His Gly Ala Val Val Asn Glu Ser His His
170 175 180

Asp Ala Leu Val Glu Asp Ile Phe Asp Lys Glu Asp Glu Asp Lys
185 190 195

Asp Gly Phe Ile Ser Ala Arg Glu Phe Thr Tyr Lys His Asp Glu
200 205 210

Leu

<210> 146

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 146

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<210> 147

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 147

gcccagagca ggaggaatga tgagc 25

<210> 148

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 148

gtggaacgcg gtcttgactc tgttcgtcac ttctttgatt ggggctttg 49

<210> 149

<211> 2196

<212> DNA

<213> Homo sapiens

<400> 149

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cagagatgcc tggctacctc gccctgcctt cagcctcacg gggctcagtc 200
tctttttctc tttggtgcc aaggagcgga gcatggaggt cacagtacct 250
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<210> 150

<211> 215

<212> PRT

<213> Homo sapiens

<400> 150

Met	His	Arg	Asp	Ala	Trp	Leu	Pro	Arg	Pro	Ala	Phe	Ser	Leu	Thr
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Gly	Leu	Ser	Leu	Phe	Phe	Ser	Leu	Val	Pro	Pro	Gly	Arg	Ser	Met
				20					25					30

Glu	Val	Thr	Val	Pro	Ala	Thr	Leu	Asn	Val	Leu	Asn	Gly	Ser	Asp
				35					40					45

Ala	Arg	Leu	Pro	Cys	Thr	Phe	Asn	Ser	Cys	Tyr	Thr	Val	Asn	His
				50					55					60

Lys	Gln	Phe	Ser	Leu	Asn	Trp	Thr	Tyr	Gln	Glu	Cys	Asn	Asn	Cys
				65					70					75

Ser	Glu	Glu	Met	Phe	Leu	Gln	Phe	Arg	Met	Lys	Ile	Ile	Asn	Leu
				80					85					90

Lys	Leu	Glu	Arg	Phe	Gln	Asp	Arg	Val	Glu	Phe	Ser	Gly	Asn	Pro
				95					100					105

Ser	Lys	Tyr	Asp	Val	Ser	Val	Met	Leu	Arg	Asn	Val	Gln	Pro	Glu
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110	115	120
Asp Glu Gly Ile Tyr Asn Cys Tyr Ile Met Asn Pro Pro Asp Arg		
125	130	135
His Arg Gly His Gly Lys Ile His Leu Gln Val Leu Met Glu Glu		
140	145	150
Pro Pro Glu Arg Asp Ser Thr Val Ala Val Ile Val Gly Ala Ser		
155	160	165
Val Gly Gly Phe Leu Ala Val Val Ile Leu Val Leu Met Val Val		
170	175	180
Lys Cys Val Arg Arg Lys Lys Glu Gln Lys Leu Ser Thr Asp Asp		
185	190	195
Leu Lys Thr Glu Glu Glu Gly Lys Thr Asp Gly Glu Gly Asn Pro		
200	205	210
Asp Asp Gly Ala Lys		
215		

<210> 151
 <211> 524
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 103, 233
 <223> unknown base

<400> 151
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 ccnactaaca tctcagtctc tgaaaatgca cagagatgcc tggctacctc 150
 gccctgcctt cagcctcacg gggctcagtc tctttttctc tttggtgcca 200
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 aatggctctg acgcccgcct gccctgcctt tcaactcctg ctacacagtg 300
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 tggagcgggt tcaagaccgc gtggagttct cagggaaccc cagcaagtac 450
 gatgtgtcgg tgatgctgag aaacgtgcag ccggaggatg aggggattta 500
 caactgctac atcatgaacc cccc 524

<210> 152

<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 56, 123
<223> unknown base

<400> 152
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ccctgaactg gatttaccag gagtgaaca actggctctg aggagatgtt 200
cctccagttc ccgcatggaa gatcatttaa cctgaaagct ggaagcgggt 250
ttcaagaacc gcgtggaagt ttctcagga accccagcaa gtacgatgtg 300
tcggtgatgc tgagaaacgt gcagccggag gatgaggga ttacaactg 350
ctacatcatg aaccccc 368

<210> 153
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 153
acggagcatg gaggtccaca gtac 24

<210> 154
<211> 23
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 154
gcacgtttct cagcatcacc gac 23

<210> 155
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 155

cgctgcct gcaccttcaa ctctgctac acagtgaacc acaaacagtt 50

<210> 156

<211> 2680

<212> DNA

<213> Homo sapiens

<400> 156

tgcggcgacc gtcgtacacc atgggcctcc acctccgccc ctaccgtgtg 50

gggctgctcc cggatggcct cctgttcttc ttgctgctgc taatgctgct 100

cgcggaacca gcgtccccg cggacgtca cccccagtg gtgctggtcc 150

ctggtgattt gggtaaccaa ctggaagcca agctggacaa gccgacagt 200

gtgcactacc tctgctccaa gaagaccgaa agctacttca caatctggct 250

gaacctggaa ctgctgctgc ctgtcatcat tgactgctgg attgacaata 300

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gtggatgtac gtgtccctgg ctttggaag accttctcac tggagttcct 400

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cagccgcagg cctggaagga caagtatatc cgggccttcg tgtcactggg 700

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<210> 157

<211> 412

<212> PRT

<213> Homo Sapien

<400> 157

Met	Gly	Leu	His	Leu	Arg	Pro	Tyr	Arg	Val	Gly	Leu	Leu	Pro	Asp
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Gly	Leu	Leu	Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Leu	Ala	Asp	Pro
				20					25					30

Ala	Leu	Pro	Ala	Gly	Arg	His	Pro	Pro	Val	Val	Leu	Val	Pro	Gly
				35					40					45

Asp	Leu	Gly	Asn	Gln	Leu	Glu	Ala	Lys	Leu	Asp	Lys	Pro	Thr	Val
				50					55					60

Val	His	Tyr	Leu	Cys	Ser	Lys	Lys	Thr	Glu	Ser	Tyr	Phe	Thr	Ile
				65					70					75

Trp	Leu	Asn	Leu	Glu	Leu	Leu	Leu	Pro	Val	Ile	Ile	Asp	Cys	Trp
				80					85					90

Ile	Asp	Asn	Ile	Arg	Leu	Val	Tyr	Asn	Lys	Thr	Ser	Arg	Ala	Thr
				95					100					105

Gln	Phe	Pro	Asp	Gly	Val	Asp	Val	Arg	Val	Pro	Gly	Phe	Gly	Lys
				110					115					120

Thr	Phe	Ser	Leu	Glu	Phe	Leu	Asp	Pro	Ser	Lys	Ser	Ser	Val	Gly
				125					130					135

Ser	Tyr	Phe	His	Thr	Met	Val	Glu	Ser	Leu	Val	Gly	Trp	Gly	Tyr
				140					145					150

Thr	Arg	Gly	Glu	Asp	Val	Arg	Gly	Ala	Pro	Tyr	Asp	Trp	Arg	Arg
				155					160					165

Ala	Pro	Asn	Glu	Asn	Gly	Pro	Tyr	Phe	Leu	Ala	Leu	Arg	Glu	Met
				170					175					180

Ile	Glu	Glu	Met	Tyr	Gln	Leu	Tyr	Gly	Gly	Pro	Val	Val	Leu	Val
				185					190					195

Ala	His	Ser	Met	Gly	Asn	Met	Tyr	Thr	Leu	Tyr	Phe	Leu	Gln	Arg
				200					205					210

Gln	Pro	Gln	Ala	Trp	Lys	Asp	Lys	Tyr	Ile	Arg	Ala	Phe	Val	Ser
				215					220					225

Leu	Gly	Ala	Pro	Trp	Gly	Gly	Val	Ala	Lys	Thr	Leu	Arg	Val	Leu
				230					235					240

Ala	Ser	Gly	Asp	Asn	Asn	Arg	Ile	Pro	Val	Ile	Gly	Pro	Leu	Lys
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245	250	255
Ile Arg Glu Gln Gln Arg Ser Ala Val	Ser Thr Ser Trp Leu	Leu
260	265	270
Pro Tyr Asn Tyr Thr Trp Ser Pro Glu	Lys Val Phe Val Gln	Thr
275	280	285
Pro Thr Ile Asn Tyr Thr Leu Arg Asp	Tyr Arg Lys Phe Phe	Gln
290	295	300
Asp Ile Gly Phe Glu Asp Gly Trp Leu	Met Arg Gln Asp Thr	Glu
305	310	315
Gly Leu Val Glu Ala Thr Met Pro Pro	Gly Val Gln Leu His	Cys
320	325	330
Leu Tyr Gly Thr Gly Val Pro Thr Pro	Asp Ser Phe Tyr Tyr	Glu
335	340	345
Ser Phe Pro Asp Arg Asp Pro Lys Ile	Cys Phe Gly Asp Gly	Asp
350	355	360
Gly Thr Val Asn Leu Lys Ser Ala Leu	Gln Cys Gln Ala Trp	Gln
365	370	375
Ser Arg Gln Glu His Gln Val Leu Leu	Gln Glu Leu Pro Gly	Ser
380	385	390
Glu His Ile Glu Met Leu Ala Asn Ala	Thr Thr Leu Ala Tyr	Leu
395	400	405
Lys Arg Val Leu Leu Gly Pro		
410		

<210> 158

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 158

ctggggctac acacggggtg agg 23

<210> 159

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 159

ggtgccgctg cagaaagtag agcg 24

<210> 160
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 160
gccccaaatg aaaacgggcc ctacttcctg gccctccgcg agatg 45

<210> 161
<211> 1512
<212> DNA
<213> Homo sapiens

<400> 161
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gcggcgcttc ctgacgcagc cgcaggtggt ggcgcgcgcc gtgtgcttgg 150
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 tgggggagat gcccggcctg ggatgctgtt tggagacgga ataaatgttt 1500
 tctcattcaa ag 1512

<210> 162
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 162
 Met Glu Ser Gly Ala Tyr Gly Ala Ala Lys Ala Gly Gly Ser Phe
 1 5 10 15
 Asp Leu Arg Arg Phe Leu Thr Gln Pro Gln Val Val Ala Arg Ala
 20 25 30
 Val Cys Leu Val Phe Ala Leu Ile Val Phe Ser Cys Ile Tyr Gly
 35 40 45
 Glu Gly Tyr Ser Asn Ala His Glu Ser Lys Gln Met Tyr Cys Val
 50 55 60
 Phe Asn Arg Asn Glu Asp Ala Cys Arg Tyr Gly Ser Ala Ile Gly
 65 70 75
 Val Leu Ala Phe Leu Ala Ser Ala Phe Phe Leu Val Val Asp Ala
 80 85 90
 Tyr Phe Pro Gln Ile Ser Asn Ala Thr Asp Arg Lys Tyr Leu Val
 95 100 105
 Ile Gly Asp Leu Leu Phe Ser Ala Leu Trp Thr Phe Leu Trp Phe
 110 115 120
 Val Gly Phe Cys Phe Leu Thr Asn Gln Trp Ala Val Thr Asn Pro
 125 130 135
 Lys Asp Val Leu Val Gly Ala Asp Ser Val Arg Ala Ala Ile Thr
 140 145 150

Phe	Ser	Phe	Phe	Ser	Ile	Phe	Ser	Trp	Gly	Val	Leu	Ala	Ser	Leu
				155					160					165
Ala	Tyr	Gln	Arg	Tyr	Lys	Ala	Gly	Val	Asp	Asp	Phe	Ile	Gln	Asn
				170					175					180
Tyr	Val	Asp	Pro	Thr	Pro	Asp	Pro	Asn	Thr	Ala	Tyr	Ala	Ser	Tyr
				185					190					195
Pro	Gly	Ala	Ser	Val	Asp	Asn	Tyr	Gln	Gln	Pro	Pro	Phe	Thr	Gln
				200					205					210
Asn	Ala	Glu	Thr	Thr	Glu	Gly	Tyr	Gln	Pro	Pro	Pro	Val	Tyr	
				215					220					

<210> 163

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 163

tggtcttcgc cttgatcgtg ttct 24

<210> 164

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 164

gtgtactgag cggcggttag 20

<210> 165

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 165

ctgaaggtga tggctgccct cac 23

<210> 166

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 166

ccaggaggct catgggaaag tcc 23

<210> 167

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 167

ccacgagtct aagcagatgt actgcgtggt caaccgcaac gaggatgcct 50

<210> 168

<211> 3143

<212> DNA

<213> Homo sapiens

<400> 168

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ctggcgggca gggggacgga ggtgatggcg aggaagcgga gccagagggg 150

atgttcaagg cctgtgagga ctccaagaga aaagcccggg gctacctccg 200

cctggtgccc ctgtttgtgc tgctggccct gctcgtgctg gcttcggcgg 250

gggtgctact ctggtatttc ctaggggtaca aggcggaggt gatggtcagc 300

caggtgtact caggcagtct gcgtgtactc aatcgccact tctcccagga 350

tcttaccgcg cggaatcta gtgccttccg cagtgaacc gccaaagccc 400

agaagatgct caaggagctc atcaccagca cccgcctggg aacttactac 450

aactccagct ccgtctattc ctttggggag ggaccctca cctgcttctt 500

ctggttcatt ctccaaatcc ccgagcaccg ccggctgatg ctgagccccg 550

aggtggtgca ggcactgctg gtggaggagc tgctgtccac agtcaacagc 600

tcggctgccg tccctacag ggccgagtac gaagtggacc ccgaggcct 650

agtgatcctg gaagccagtg tgaaagacat agctgcattg aattccacgc 700

tgggttggtta ccgtacagc tacgtgggcc agggccaggt cctccggctg 750

aaggggcctg accacctggc ctccagctgc ctgtggcacc tgcagggccc 800

caaggacctc atgtctaaac tccggctgga gtggacgctg gcagagtgcc 850

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atcacctcgg tgtacggctg cagccgccag gagcccgtgg tggaggttct 950

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aagggtgtgg agaactcgcg ctggcctgga gaggtgtcct tcaaggtgag 2000
ccgcctgctc ctgcacccgt accacgaaga ggacagccat gactacgacg 2050
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cccgctctgc tgcccgcgcg ctcccacttc ttcgagcccg gcctgactg 2150
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 tttggaataa agctgcctga tcaaaaaaaaa aaaaaaaaaa aaa 3143

<210> 169
 <211> 802
 <212> PRT
 <213> Homo sapiens

<400> 169
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 Gly Gly Asp Gly Glu Glu Ala Glu Pro Glu Gly Met Phe Lys Ala
 20 25 30
 Cys Glu Asp Ser Lys Arg Lys Ala Arg Gly Tyr Leu Arg Leu Val
 35 40 45
 Pro Leu Phe Val Leu Leu Ala Leu Leu Val Leu Ala Ser Ala Gly
 50 55 60
 Val Leu Leu Trp Tyr Phe Leu Gly Tyr Lys Ala Glu Val Met Val
 65 70 75
 Ser Gln Val Tyr Ser Gly Ser Leu Arg Val Leu Asn Arg His Phe
 80 85 90
 Ser Gln Asp Leu Thr Arg Arg Glu Ser Ser Ala Phe Arg Ser Glu

	95	100	105
Thr Ala Lys Ala Gln Lys Met Leu Lys Glu Leu Ile Thr Ser Thr	110	115	120
Arg Leu Gly Thr Tyr Tyr Asn Ser Ser Ser Val Tyr Ser Phe Gly	125	130	135
Glu Gly Pro Leu Thr Cys Phe Phe Trp Phe Ile Leu Gln Ile Pro	140	145	150
Glu His Arg Arg Leu Met Leu Ser Pro Glu Val Val Gln Ala Leu	155	160	165
Leu Val Glu Glu Leu Leu Ser Thr Val Asn Ser Ser Ala Ala Val	170	175	180
Pro Tyr Arg Ala Glu Tyr Glu Val Asp Pro Glu Gly Leu Val Ile	185	190	195
Leu Glu Ala Ser Val Lys Asp Ile Ala Ala Leu Asn Ser Thr Leu	200	205	210
Gly Cys Tyr Arg Tyr Ser Tyr Val Gly Gln Gly Gln Val Leu Arg	215	220	225
Leu Lys Gly Pro Asp His Leu Ala Ser Ser Cys Leu Trp His Leu	230	235	240
Gln Gly Pro Lys Asp Leu Met Leu Lys Leu Arg Leu Glu Trp Thr	245	250	255
Leu Ala Glu Cys Arg Asp Arg Leu Ala Met Tyr Asp Val Ala Gly	260	265	270
Pro Leu Glu Lys Arg Leu Ile Thr Ser Val Tyr Gly Cys Ser Arg	275	280	285
Gln Glu Pro Val Val Glu Val Leu Ala Ser Gly Ala Ile Met Ala	290	295	300
Val Val Trp Lys Lys Gly Leu His Ser Tyr Tyr Asp Pro Phe Val	305	310	315
Leu Ser Val Gln Pro Val Val Phe Gln Ala Cys Glu Val Asn Leu	320	325	330
Thr Leu Asp Asn Arg Leu Asp Ser Gln Gly Val Leu Ser Thr Pro	335	340	345
Tyr Phe Pro Ser Tyr Tyr Ser Pro Gln Thr His Cys Ser Trp His	350	355	360
Leu Thr Val Pro Ser Leu Asp Tyr Gly Leu Ala Leu Trp Phe Asp	365	370	375
Ala Tyr Ala Leu Arg Arg Gln Lys Tyr Asp Leu Pro Cys Thr Gln			

380					385					390				
Gly	Gln	Trp	Thr	Ile	Gln	Asn	Arg	Arg	Leu	Cys	Gly	Leu	Arg	Ile
				395					400					405
Leu	Gln	Pro	Tyr	Ala	Glu	Arg	Ile	Pro	Val	Val	Ala	Thr	Ala	Gly
				410					415					420
Ile	Thr	Ile	Asn	Phe	Thr	Ser	Gln	Ile	Ser	Leu	Thr	Gly	Pro	Gly
				425					430					435
Val	Arg	Val	His	Tyr	Gly	Leu	Tyr	Asn	Gln	Ser	Asp	Pro	Cys	Pro
				440					445					450
Gly	Glu	Phe	Leu	Cys	Ser	Val	Asn	Gly	Leu	Cys	Val	Pro	Ala	Cys
				455					460					465
Asp	Gly	Val	Lys	Asp	Cys	Pro	Asn	Gly	Leu	Asp	Glu	Arg	Asn	Cys
				470					475					480
Val	Cys	Arg	Ala	Thr	Phe	Gln	Cys	Lys	Glu	Asp	Ser	Thr	Cys	Ile
				485					490					495
Ser	Leu	Pro	Lys	Val	Cys	Asp	Gly	Gln	Pro	Asp	Cys	Leu	Asn	Gly
				500					505					510
Ser	Asp	Glu	Glu	Gln	Cys	Gln	Glu	Gly	Val	Pro	Cys	Gly	Thr	Phe
				515					520					525
Thr	Phe	Gln	Cys	Glu	Asp	Arg	Ser	Cys	Val	Lys	Lys	Pro	Asn	Pro
				530					535					540
Gln	Cys	Asp	Gly	Arg	Pro	Asp	Cys	Arg	Asp	Gly	Ser	Asp	Glu	Glu
				545					550					555
His	Cys	Asp	Cys	Gly	Leu	Gln	Gly	Pro	Ser	Ser	Arg	Ile	Val	Gly
				560					565					570
Gly	Ala	Val	Ser	Ser	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu
				575					580					585
Gln	Val	Arg	Gly	Arg	His	Ile	Cys	Gly	Gly	Ala	Leu	Ile	Ala	Asp
				590					595					600
Arg	Trp	Val	Ile	Thr	Ala	Ala	His	Cys	Phe	Gln	Glu	Asp	Ser	Met
				605					610					615
Ala	Ser	Thr	Val	Leu	Trp	Thr	Val	Phe	Leu	Gly	Lys	Val	Trp	Gln
				620					625					630
Asn	Ser	Arg	Trp	Pro	Gly	Glu	Val	Ser	Phe	Lys	Val	Ser	Arg	Leu
				635					640					645
Leu	Leu	His	Pro	Tyr	His	Glu	Glu	Asp	Ser	His	Asp	Tyr	Asp	Val
				650					655					660
Ala	Leu	Leu	Gln	Leu	Asp	His	Pro	Val	Val	Arg	Ser	Ala	Ala	Val

665					670					675				
Arg	Pro	Val	Cys	Leu	Pro	Ala	Arg	Ser	His	Phe	Phe	Glu	Pro	Gly
				680					685					690
Leu	His	Cys	Trp	Ile	Thr	Gly	Trp	Gly	Ala	Leu	Arg	Glu	Gly	Gly
				695					700					705
Pro	Ile	Ser	Asn	Ala	Leu	Gln	Lys	Val	Asp	Val	Gln	Leu	Ile	Pro
				710					715					720
Gln	Asp	Leu	Cys	Ser	Glu	Ala	Tyr	Arg	Tyr	Gln	Val	Thr	Pro	Arg
				725					730					735
Met	Leu	Cys	Ala	Gly	Tyr	Arg	Lys	Gly	Lys	Lys	Asp	Ala	Cys	Gln
				740					745					750
Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Lys	Ala	Leu	Ser	Gly	Arg
				755					760					765
Trp	Phe	Leu	Ala	Gly	Leu	Val	Ser	Trp	Gly	Leu	Gly	Cys	Gly	Arg
				770					775					780
Pro	Asn	Tyr	Phe	Gly	Val	Tyr	Thr	Arg	Ile	Thr	Gly	Val	Ile	Ser
				785					790					795
Trp	Ile	Gln	Gln	Val	Val	Thr								
				800										

<210> 170

<211> 1327

<212> DNA

<213> Homo sapiens

<400> 170

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tgcactatgg cttgtacaac cagtcggacc cctgccctgg agagttcctc 200

tgttctgtga atggactctg tgtccctgcc tgtgatgggg tcaaggactg 250

ccccaacggc ctggatgaga gaaactgcgt ttgcagagcc acattccagt 300

gcaaagagga cagcacatgc atctcactgc ccaaggtctg tgatgggcag 350

cctgattgtc tcaacggcag cgatgaagag cagtgccagg aaggggtgcc 400

atgtgggaca ttcaccttcc agtgtgagga ccggagctgc gtgaagaagc 450

ccaacccgca gtgtgatggg cggcccgact gcagggacgg ctcgatgag 500

gagcactgtg actgtggcct ccagggcccc tccagccgca ttgttggtgg 550

agctgtgtcc tccgaggggtg agtggccatg gcaggccagc ctccaggttc 600
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 gaccgtgttc ctgggcaagg tgtggcagaa ctgcgctgg cctggagagg 750
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 gtgccggcta ccgcaagggc aagaaggatg cctgtcaggg tgactcaggt 1100
 ggtccgctgg tgtgcaaggc actcagtggc cgctggttcc tggcggggct 1150
 ggtcagctgg ggctgggct gtggccggcc taactacttc ggcgtctaca 1200
 cccgcatcac aggtgtgatc agctggatcc agcaagtggg gacctgagga 1250
 actgcccccc tgcaaagcag ggcccacctc ctggactcag agagcccagg 1300
 gcaactgcca agcaggggga caagtat 1327

<210> 171

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

taacagctgc ccactgcttc cagg 24

<210> 172

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 172

taatccagca gtgcaggccg gg 22

<210> 173

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 173

atggcctcca cgggtgctgtg gaccgtgttc ctgggcaagg tgtggcagaa 50

<210> 174

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 174

tgcctatgca ctgaggaggc agaag 25

<210> 175

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 175

aggcagggac acagagtcca ttcac 25

<210> 176

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 176

agtatgattt gccgtgcacc cagggccagt ggacgatcca gaacaggagg 50

<210> 177

<211> 1510

<212> DNA

<213> Homo sapiens

<400> 177

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ccaccgcccg ggctccgtgc cgccaagttt tcattttcca ctttctctgc 100

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gctggaaaca ccaagagggtg gtttttgttt tttaaaactt ctgtttcttg 200

ggaggggggtg tggcggggca ggatgagcaa ctccgttcct ctgctctgtt 250

tctggagcct ctgctattgc tttgctgcg ggagccccgt accttttgg 300
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cagcattgcc aggatgctcg actggctgca ggagaaggac gatttttctc 700
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cggacgatgc agattttgtg gatgtcctcc acacctacac gcgttccttc 900
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caattgcata tggaacaatc acagaggtgg taaaatgtga gcatgagcga 1050
gccgtccacc tctttgttga ctctctggtg aatcaggaca agccgagttt 1100
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agaagtggcc agcacaatcc aatcaaatcg ttgcaaata gattacactg 1400
tgcatgtcct aggaaaggga atctttacaa aataaacagt gtggaccct 1450
aataaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500
aaaaaaaaa 1510

<210> 178
<211> 354
<212> PRT
<213> Homo sapiens

<400> 178

Met	Ser	Asn	Ser	Val	Pro	Leu	Leu	Cys	Phe	Trp	Ser	Leu	Cys	Tyr	
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Cys	Phe	Ala	Ala	Gly	Ser	Pro	Val	Pro	Phe	Gly	Pro	Glu	Gly	Arg	
				20					25					30	
Leu	Glu	Asp	Lys	Leu	His	Lys	Pro	Lys	Ala	Thr	Gln	Thr	Glu	Val	
				35					40					45	
Lys	Pro	Ser	Val	Arg	Phe	Asn	Leu	Arg	Thr	Ser	Lys	Asp	Pro	Glu	
				50					55					60	
His	Glu	Gly	Cys	Tyr	Leu	Ser	Val	Gly	His	Ser	Gln	Pro	Leu	Glu	
				65					70					75	
Asp	Cys	Ser	Phe	Asn	Met	Thr	Ala	Lys	Thr	Phe	Phe	Ile	Ile	His	
				80					85					90	
Gly	Trp	Thr	Met	Ser	Gly	Ile	Phe	Glu	Asn	Trp	Leu	His	Lys	Leu	
				95					100					105	
Val	Ser	Ala	Leu	His	Thr	Arg	Glu	Lys	Asp	Ala	Asn	Val	Val	Val	
				110					115					120	
Val	Asp	Trp	Leu	Pro	Leu	Ala	His	Gln	Leu	Tyr	Thr	Asp	Ala	Val	
				125					130					135	
Asn	Asn	Thr	Arg	Val	Val	Gly	His	Ser	Ile	Ala	Arg	Met	Leu	Asp	
				140					145					150	
Trp	Leu	Gln	Glu	Lys	Asp	Asp	Phe	Ser	Leu	Gly	Asn	Val	His	Leu	
				155					160					165	
Ile	Gly	Tyr	Ser	Leu	Gly	Ala	His	Val	Ala	Gly	Tyr	Ala	Gly	Asn	
				170					175					180	
Phe	Val	Lys	Gly	Thr	Val	Gly	Arg	Ile	Thr	Gly	Leu	Asp	Pro	Ala	
				185					190					195	
Gly	Pro	Met	Phe	Glu	Gly	Ala	Asp	Ile	His	Lys	Arg	Leu	Ser	Pro	
				200					205					210	
Asp	Asp	Ala	Asp	Phe	Val	Asp	Val	Leu	His	Thr	Tyr	Thr	Arg	Ser	
				215					220					225	
Phe	Gly	Leu	Ser	Ile	Gly	Ile	Gln	Met	Pro	Val	Gly	His	Ile	Asp	
				230					235					240	
Ile	Tyr	Pro	Asn	Gly	Gly	Asp	Phe	Gln	Pro	Gly	Cys	Gly	Leu	Asn	
				245					250					255	
Asp	Val	Leu	Gly	Ser	Ile	Ala	Tyr	Gly	Thr	Ile	Thr	Glu	Val	Val	
				260					265					270	
Lys	Cys	Glu	His	Glu	Arg	Ala	Val	His	Leu	Phe	Val	Asp	Ser	Leu	
				275					280					285	

Val Asn Gln Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser
290 295 300

Asn Arg Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg
305 310 315

Cys Asn Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg
320 325 330

Asn Ser Lys Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe Arg
335 340 345

Gly Asn Leu Gln Ser Leu Glu Cys Pro
350

<210> 179

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 179

gtgagcatga gcgagccgtc cac 23

<210> 180

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 180

gctattacaa cggttcttgc ggcagc 26

<210> 181

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 181

ttgactctct ggtgaatcag gacaagccga gttttgcctt ccag 44

<210> 182

<211> 3240

<212> DNA

<213> Homo sapiens

<400> 182

cggacgcgtg ggcggacgcg tgggcctggg caagggccgg ggcgccgggc 50

cgagccacct cttccctccc cccgcttccc tgtcgcgctc cgctggctgg 100
acgcgctgga ggagtggagc agcaccggc cgccctggg ggctgacagt 150
cggcaaagtt tggcccgaag aggaagtggc ctcaaacc cgcaggtggc 200
gaccaggcca gaccaggggc gctcgcctgc tgcgggcggg ctgtaggcga 250
gggcgcgccc cagtgccgag acccggggct tcaggagccg gccccgggag 300
agaagagtgc ggcggcggac ggagaaaaca actccaaagt tggcgaaagg 350
caccgcccct actccgggc tgccgccgc tccccgccc cagccctggc 400
atccagagta cgggtcgagc ccgggccatg gagccccct ggggaggcgg 450
caccagggag cctgggcgcc cggggctccg ccgcgacccc atcgggtaga 500
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ccaccatttg ggtggctggt tttaaaaagt aaagttctta gaggatcata 3000
ggtctggaca ctccatcctt gccaaacctc tacccaaaag tggccttaag 3050
caccggaatg ccaattaact agagaccctc cagcccccaa ggggaggatt 3100
tgggcagaac ctgaggtttt gccatccaca atccctccta cagggcctgg 3150
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tcagtaagtt gaggtcaaaa ataaaggaat catacatctc 3240

<210> 183

<211> 713

<212> PRT

<213> Homo sapiens

<400> 183

Met	Leu	Leu	Ala	Thr	Leu	Leu	Leu	Leu	Leu	Gly	Gly	Ala	Leu	1	5	10	15
Ala	His	Pro	Asp	Arg	Ile	Ile	Phe	Pro	Asn	His	Ala	Cys	Glu	Asp	20	25	30
Pro	Pro	Ala	Val	Leu	Leu	Glu	Val	Gln	Gly	Thr	Leu	Gln	Arg	Pro	35	40	45
Leu	Val	Arg	Asp	Ser	Arg	Thr	Ser	Pro	Ala	Asn	Cys	Thr	Trp	Leu	50	55	60
Ile	Leu	Gly	Ser	Lys	Glu	Gln	Thr	Val	Thr	Ile	Arg	Phe	Gln	Lys	65	70	75
Leu	His	Leu	Ala	Cys	Gly	Ser	Glu	Arg	Leu	Thr	Leu	Arg	Ser	Pro	80	85	90
Leu	Gln	Pro	Leu	Ile	Ser	Leu	Cys	Glu	Ala	Pro	Pro	Ser	Pro	Leu	95	100	105
Gln	Leu	Pro	Gly	Gly	Asn	Val	Thr	Ile	Thr	Tyr	Ser	Tyr	Ala	Gly	110	115	120
Ala	Arg	Ala	Pro	Met	Gly	Gln	Gly	Phe	Leu	Leu	Ser	Tyr	Ser	Gln	125	130	135
Asp	Trp	Leu	Met	Cys	Leu	Gln	Glu	Glu	Phe	Gln	Cys	Leu	Asn	His	140	145	150
Arg	Cys	Val	Ser	Ala	Val	Gln	Arg	Cys	Asp	Gly	Val	Asp	Ala	Cys	155	160	165
Gly	Asp	Gly	Ser	Asp	Glu	Ala	Gly	Cys	Ser	Ser	Asp	Pro	Phe	Pro	170	175	180
Gly	Leu	Thr	Pro	Arg	Pro	Val	Pro	Ser	Leu	Pro	Cys	Asn	Val	Thr			

185	190	195
Leu Glu Asp Phe Tyr Gly Val Phe Ser	Ser Pro Gly Tyr Thr His	
200	205	210
Leu Ala Ser Val Ser His Pro Gln Ser	Cys His Trp Leu Leu Asp	
215	220	225
Pro His Asp Gly Arg Arg Leu Ala Val	Arg Phe Thr Ala Leu Asp	
230	235	240
Leu Gly Phe Gly Asp Ala Val His Val	Tyr Asp Gly Pro Gly Pro	
245	250	255
Pro Glu Ser Ser Arg Leu Leu Arg Ser	Leu Thr His Phe Ser Asn	
260	265	270
Gly Lys Ala Val Thr Val Glu Thr Leu	Ser Gly Gln Ala Val Val	
275	280	285
Ser Tyr His Thr Val Ala Trp Ser Asn	Gly Arg Gly Phe Asn Ala	
290	295	300
Thr Tyr His Val Arg Gly Tyr Cys Leu	Pro Trp Asp Arg Pro Cys	
305	310	315
Gly Leu Gly Ser Gly Leu Gly Ala Gly	Glu Gly Leu Gly Glu Arg	
320	325	330
Cys Tyr Ser Glu Ala Gln Arg Cys Asp	Gly Ser Trp Asp Cys Ala	
335	340	345
Asp Gly Thr Asp Glu Glu Asp Cys Pro	Gly Cys Pro Pro Gly His	
350	355	360
Phe Pro Cys Gly Ala Ala Gly Thr Ser	Gly Ala Thr Ala Cys Tyr	
365	370	375
Leu Pro Ala Asp Arg Cys Asn Tyr Gln	Thr Phe Cys Ala Asp Gly	
380	385	390
Ala Asp Glu Arg Arg Cys Arg His Cys	Gln Pro Gly Asn Phe Arg	
395	400	405
Cys Arg Asp Glu Lys Cys Val Tyr Glu	Thr Trp Val Cys Asp Gly	
410	415	420
Gln Pro Asp Cys Ala Asp Gly Ser Asp	Glu Trp Asp Cys Ser Tyr	
425	430	435
Val Leu Pro Arg Lys Val Ile Thr Ala	Ala Val Ile Gly Ser Leu	
440	445	450
Val Cys Gly Leu Leu Leu Val Ile Ala	Leu Gly Cys Thr Cys Lys	
455	460	465
Leu Tyr Ala Ile Arg Thr Gln Glu Tyr	Ser Ile Phe Ala Pro Leu	

470										475					480				
Ser	Arg	Met	Glu	Ala	Glu	Ile	Val	Gln	Gln	Gln	Ala	Pro	Pro	Ser					
				485					490					495					
Tyr	Gly	Gln	Leu	Ile	Ala	Gln	Gly	Ala	Ile	Pro	Pro	Val	Glu	Asp					
				500					505					510					
Phe	Pro	Thr	Glu	Asn	Pro	Asn	Asp	Asn	Ser	Val	Leu	Gly	Asn	Leu					
				515					520					525					
Arg	Ser	Leu	Leu	Gln	Ile	Leu	Arg	Gln	Asp	Met	Thr	Pro	Gly	Gly					
				530					535					540					
Gly	Pro	Gly	Ala	Arg	Arg	Arg	Gln	Arg	Gly	Arg	Leu	Met	Arg	Arg					
				545					550					555					
Leu	Val	Arg	Arg	Leu	Arg	Arg	Trp	Gly	Leu	Leu	Pro	Arg	Thr	Asn					
				560					565					570					
Thr	Pro	Ala	Arg	Ala	Ser	Glu	Ala	Arg	Ser	Gln	Val	Thr	Pro	Ser					
				575					580					585					
Ala	Ala	Pro	Leu	Glu	Ala	Leu	Asp	Gly	Gly	Thr	Gly	Pro	Ala	Arg					
				590					595					600					
Glu	Gly	Gly	Ala	Val	Gly	Gly	Gln	Asp	Gly	Glu	Gln	Ala	Pro	Pro					
				605					610					615					
Leu	Pro	Ile	Lys	Ala	Pro	Leu	Pro	Ser	Ala	Ser	Thr	Ser	Pro	Ala					
				620					625					630					
Pro	Thr	Thr	Val	Pro	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Ser	Leu	Pro					
				635					640					645					
Leu	Glu	Pro	Ser	Leu	Leu	Ser	Gly	Val	Val	Gln	Ala	Leu	Arg	Gly					
				650					655					660					
Arg	Leu	Leu	Pro	Ser	Leu	Gly	Pro	Pro	Gly	Pro	Thr	Arg	Ser	Pro					
				665					670					675					
Pro	Gly	Pro	His	Thr	Ala	Val	Leu	Ala	Leu	Glu	Asp	Glu	Asp	Asp					
				680					685					690					
Val	Leu	Leu	Val	Pro	Leu	Ala	Glu	Pro	Gly	Val	Trp	Val	Ala	Glu					
				695					700					705					
Ala	Glu	Asp	Glu	Pro	Leu	Leu	Thr												
				710															

<210> 184

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 184
ggctgtcact gtggagacac 20

<210> 185
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 185
gcaagggtcat tacagctg 18

<210> 186
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 186
agaacatagg agcagtccca ctc 23

<210> 187
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 187
tgcctgctgc tgcacaatct cag 23

<210> 188
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 188
ggctattgct tgccttgga cagaccctgt ggcttaggct ctggc 45

<210> 189
<211> 663
<212> DNA
<213> Homo sapiens

<400> 189
cgagctgggc gagaagtagg ggagggcggt gctccgccgc ggtggcggtt 50
gctatcgctt cgcagaacct actcaggcag ccagctgaga agagttgagg 100

gaaagtgctg ctgctgggtc tgcagacgcg atggataacg tgcagccgaa 150
 aataaaacat cgtcccttct gcttcagtgt gaaaggccac gtgaagatgc 200
 tgcggctggc actaactgtg acatctatga ccttttttat catcgacaaa 250
 gccctgaac catatattgt tatcactgga tttgaagtca ccgttatctt 300
 atttttcata cttttatatg tactcagact tgatcgatta atgaagtggg 350
 tattttggcc tttgcttgat attatcaact cactggtaac aacagtattc 400
 atgctcatcg tatctgtgtt ggcactgata ccagaaacca caacattgac 450
 agttggtgga ggggtgtttg cacttgtgac agcagtatgc tgtcttgccg 500
 acggggccct tatttaccgg aagcttctgt tcaatcccag cggtccttac 550
 cagaaaaagc ctgtgcatga aaaaaaagaa gttttgtaat tttatattac 600
 ttttagttt gatactaagt attaaacata tttctgtatt cttccaaaaa 650
 aaaaaaaaaa aaa 663

<210> 190
 <211> 152
 <212> PRT
 <213> Homo sapiens

<400> 190
 Met Asp Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe
 1 5 10 15
 Ser Val Lys Gly His Val Lys Met Leu Arg Leu Ala Leu Thr Val
 20 25 30
 Thr Ser Met Thr Phe Phe Ile Ile Ala Gln Ala Pro Glu Pro Tyr
 35 40 45
 Ile Val Ile Thr Gly Phe Glu Val Thr Val Ile Leu Phe Phe Ile
 50 55 60
 Leu Leu Tyr Val Leu Arg Leu Asp Arg Leu Met Lys Trp Leu Phe
 65 70 75
 Trp Pro Leu Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Phe
 80 85 90
 Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr
 95 100 105
 Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys
 110 115 120
 Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn
 125 130 135

Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu
140 145 150

Val Leu

<210> 191

<211> 495

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 78, 212, 234, 487

<223> unknown base

<400> 191

gggcgagaag taggggaggg cgtgttccgc cgcggtggcg gttgctatcg 50

ttttgcagaa cctactcagg cagccagntg agaagagttg agggaaagtg 100

ctgctgctgg gtctgcagac gcgatggata acgtgcagcc gaaaataaaa 150

catcgcccct tctgcttcag tgtgaaaggc cacgtgaaga tgctgcggct 200

ggcactaact gngacatcta tgaccttttt tatnatcgca caagcccctg 250

aaccatatat tgttatcact ggatttgaag tcaccgttat cttatttttc 300

atacttttat atgtactcag acttgatcga ttaatgaagt ggttattttg 350

gcctttgctt gatattatca actcactggg aacaacagta ttcattgctca 400

tcgtatctgt gttggcactg ataccagaaa ccacaacatt gacagttggg 450

ggaggggtgt ttgcacttgt gacagcagta tgctgtnttg ccgac 495

<210> 192

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 192

cgttttgcag aacctactca ggcag 25

<210> 193

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 193

cctccaccaa ctgtcaatgt tgtgg 25

<210> 194

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 194

aaagtgtgtc tgctgggtct gcagacgcga tggataacgt 40

<210> 195

<211> 1879

<212> DNA

<213> Homo sapien

<400> 195

cagccccgcg cgccggccga gtcgtgagc cgcggtgcc ggacgggacg 50

ggaccggcta ggctgggagc gcccccgagg ccccgccgtg ggcattggcg 100

cactggcccc ggcgctgctg ctgcctctgc tggcccagtg gctcctgcgc 150

gccgccccgg agctggcccc cgcgcccttc acgctgcccc tccgggtggc 200

cgcgggccacg aaccgcgtag ttgcgcccac cccgggaccc gggacccttg 250

ccgagcgcca cgccgacggc ttggcgctcg ccctggagcc tgccttggcg 300

tcccccgagg gcgcccga cttcttggcc atggtagaca acctgcaggg 350

ggactctggc cgcggtact acctggagat gctgatcggg accccccgcg 400

agaagctaca gattctcggt gacactggaa gcagtaactt tgccgtggca 450

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cacataccgc tccaagggct ttgacgtcac agtgaagtac acacaaggaa 550

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aatacttctt ttcttgtcaa cattgccact atttttgaat cagagaattt 650

ctttttgcct gggattaaat ggaatggaat acttggccta gcttatgcca 700

cacttgccaa gccatcaagt tctctggaga ctttcttcga ctccctgggtg 750

acacaagcaa acatcccccga cgttttctcc atgcagatgt gtggagcccg 800

cttgcccgtt gctggatctg ggaccaacgg aggtagtctt gtcttgggtg 850

gaattgaacc aagtttgtat aaaggagaca tctggtatac ccctattaag 900

gaagagtggg actaccagat agaaattctg aaattggaaa ttggaggcca 950

aagccttaat ctggactgca gagagtataa cgcagacaag gccatcgtgg 1000
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gtggaagctg tggcccgccg atctctgatt ccagaattct ctgatgggtt 1100
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attgtgtcct atgcgctcat gagcgtctgt ggagccatcc tccttgtctt 1550
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ctgaggtcgt caatgatgag tcctctctgg tcagacatcg ctggaaatga 1650
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caccgtctt caatctctgt tctgctccca gatgccttct agattcactg 1800
tcttttgatt cttgattttc aagctttcaa atcctcccta cttccaagaa 1850
aaataattaa aaaaaaaact tcattctaa 1879

<210> 196

<211> 518

<212> PRT.

<213> Homo sapien

<400> 196

Met	Gly	Ala	Leu	Ala	Arg	Ala	Leu	Leu	Leu	Pro	Leu	Leu	Ala	Gln
1				5					10					15

Trp	Leu	Leu	Arg	Ala	Ala	Pro	Glu	Leu	Ala	Pro	Ala	Pro	Phe	Thr
			20						25					30

Leu	Pro	Leu	Arg	Val	Ala	Ala	Ala	Thr	Asn	Arg	Val	Val	Ala	Pro
			35						40					45

Thr	Pro	Gly	Pro	Gly	Thr	Pro	Ala	Glu	Arg	His	Ala	Asp	Gly	Leu
			50						55					60

Ala	Leu	Ala	Leu	Glu 65	Pro	Ala	Leu	Ala	Ser 70	Pro	Ala	Gly	Ala	Ala 75
Asn	Phe	Leu	Ala	Met 80	Val	Asp	Asn	Leu	Gln 85	Gly	Asp	Ser	Gly	Arg 90
Gly	Tyr	Tyr	Leu	Glu 95	Met	Leu	Ile	Gly	Thr 100	Pro	Pro	Gln	Lys	Leu 105
Gln	Ile	Leu	Val	Asp 110	Thr	Gly	Ser	Ser	Asn 115	Phe	Ala	Val	Ala	Gly 120
Thr	Pro	His	Ser	Tyr 125	Ile	Asp	Thr	Tyr	Phe 130	Asp	Thr	Glu	Arg	Ser 135
Ser	Thr	Tyr	Arg	Ser 140	Lys	Gly	Phe	Asp	Val 145	Thr	Val	Lys	Tyr	Thr 150
Gln	Gly	Ser	Trp	Thr 155	Gly	Phe	Val	Gly	Glu 160	Asp	Leu	Val	Thr	Ile 165
Pro	Lys	Gly	Phe	Asn 170	Thr	Ser	Phe	Leu	Val 175	Asn	Ile	Ala	Thr	Ile 180
Phe	Glu	Ser	Glu	Asn 185	Phe	Phe	Leu	Pro	Gly 190	Ile	Lys	Trp	Asn	Gly 195
Ile	Leu	Gly	Leu	Ala 200	Tyr	Ala	Thr	Leu	Ala 205	Lys	Pro	Ser	Ser	Ser 210
Leu	Glu	Thr	Phe	Phe 215	Asp	Ser	Leu	Val	Thr 220	Gln	Ala	Asn	Ile	Pro 225
Asn	Val	Phe	Ser	Met 230	Gln	Met	Cys	Gly	Ala 235	Gly	Leu	Pro	Val	Ala 240
Gly	Ser	Gly	Thr	Asn 245	Gly	Gly	Ser	Leu	Val 250	Leu	Gly	Gly	Ile	Glu 255
Pro	Ser	Leu	Tyr	Lys 260	Gly	Asp	Ile	Trp	Tyr 265	Thr	Pro	Ile	Lys	Glu 270
Glu	Trp	Tyr	Tyr	Gln 275	Ile	Glu	Ile	Leu	Lys 280	Leu	Glu	Ile	Gly	Gly 285
Gln	Ser	Leu	Asn	Leu 290	Asp	Cys	Arg	Glu	Tyr 295	Asn	Ala	Asp	Lys	Ala 300
Ile	Val	Asp	Ser	Gly 305	Thr	Thr	Leu	Leu	Arg 310	Leu	Pro	Gln	Lys	Val 315
Phe	Asp	Ala	Val	Val 320	Glu	Ala	Val	Ala	Arg 325	Ala	Ser	Leu	Ile	Pro 330
Glu	Phe	Ser	Asp	Gly 335	Phe	Trp	Thr	Gly	Ser 340	Gln	Leu	Ala	Cys	Trp 345

Thr Asn Ser Glu	Thr Pro Trp Ser Tyr	Phe Pro Lys Ile Ser	Ile
350		355	360
Tyr Leu Arg Asp	Glu Asn Ser Ser Arg	Ser Phe Arg Ile Thr	Ile
365		370	375
Leu Pro Gln Leu	Tyr Ile Gln Pro Met	Met Gly Ala Gly Leu	Asn
380		385	390
Tyr Glu Cys Tyr	Arg Phe Gly Ile Ser	Pro Ser Thr Asn Ala	Leu
395		400	405
Val Ile Gly Ala	Thr Val Met Glu Gly	Phe Tyr Val Ile Phe	Asp
410		415	420
Arg Ala Gln Lys	Arg Val Gly Phe Ala	Ala Ser Pro Cys Ala	Glu
425		430	435
Ile Ala Gly Ala	Ala Val Ser Glu Ile	Ser Gly Pro Phe Ser	Thr
440		445	450
Glu Asp Val Ala	Ser Asn Cys Val Pro	Ala Gln Ser Leu Ser	Glu
455		460	465
Pro Ile Leu Trp	Ile Val Ser Tyr Ala	Leu Met Ser Val Cys	Gly
470		475	480
Ala Ile Leu Leu	Val Leu Ile Val Leu	Leu Leu Leu Pro Phe	Arg
485		490	495
Cys Gln Arg Arg	Pro Arg Asp Pro Glu	Val Val Asn Asp Glu	Ser
500		505	510
Ser Leu Val Arg	His Arg Trp Lys		
515			

<210> 197

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 197

cgcagaagct acagattctc g 21

<210> 198

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 198

ggaaattgga ggccaaagc 19

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<212> DNA
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<400> 199
ggatgtagcc agcaactgtg 20

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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 200
gccttggtc gttctcttc 19

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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 201
ggtcctgtgc ctggatgg 18

<210> 202
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 202
gacaagacta cctccgttgg tc 22

<210> 203
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 203
tgatgcacag ttcagcacct gttg 24

<210> 204

<211> 47
<212> DNA
<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 204
cgctccaagg gctttgacgt cacagtgaag tacacacaag gaagctg 47

<210> 205
<211> 1939
<212> DNA
<213> Homo sapiens

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cgctccgcc ttcggaggct gacgcgccg ggcgcggttc caggcctgtg 50
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 ttccgggagg atgcagggtt ggggtcatct gtatctgaag cccctcggaa 1900
 taaagcgcgt tgaccgccaa aaaaaaaaaa aaaaaaaaaa 1939

<210> 206

<211> 377

<212> PRT

<213> Homo sapiens

<400> 206

Met	Glu	Ala	Leu	Leu	Leu	Gly	Ala	Gly	Leu	Leu	Leu	Gly	Ala	Tyr
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Val	Leu	Val	Tyr	Tyr	Asn	Leu	Val	Lys	Ala	Pro	Pro	Cys	Gly	Gly
				20					25					30

Met	Gly	Asn	Leu	Arg	Gly	Arg	Thr	Ala	Val	Val	Thr	Gly	Ala	Asn
				35					40					45

Ser	Gly	Ile	Gly	Lys	Met	Thr	Ala	Leu	Glu	Leu	Ala	Arg	Arg	Gly
				50					55					60

Ala	Arg	Val	Val	Leu	Ala	Cys	Arg	Ser	Gln	Glu	Arg	Gly	Glu	Ala
				65					70					75

Ala	Ala	Phe	Asp	Leu	Arg	Gln	Glu	Ser	Gly	Asn	Asn	Glu	Val	Ile	80	85	90
Phe	Met	Ala	Leu	Asp	Leu	Ala	Ser	Leu	Ala	Ser	Val	Arg	Ala	Phe	95	100	105
Ala	Thr	Ala	Phe	Leu	Ser	Ser	Glu	Pro	Arg	Leu	Asp	Ile	Leu	Ile	110	115	120
His	Asn	Ala	Gly	Ile	Ser	Ser	Cys	Gly	Arg	Thr	Arg	Glu	Ala	Phe	125	130	135
Asn	Leu	Leu	Leu	Arg	Val	Asn	His	Ile	Gly	Pro	Phe	Leu	Leu	Thr	140	145	150
His	Leu	Leu	Leu	Pro	Cys	Leu	Lys	Ala	Cys	Ala	Pro	Ser	Arg	Val	155	160	165
Val	Val	Val	Ala	Ser	Ala	Ala	His	Cys	Arg	Gly	Arg	Leu	Asp	Phe	170	175	180
Lys	Arg	Leu	Asp	Arg	Pro	Val	Val	Gly	Trp	Arg	Gln	Glu	Leu	Arg	185	190	195
Ala	Tyr	Ala	Asp	Thr	Lys	Leu	Ala	Asn	Val	Leu	Phe	Ala	Arg	Glu	200	205	210
Leu	Ala	Asn	Gln	Leu	Glu	Ala	Thr	Gly	Val	Thr	Cys	Tyr	Ala	Ala	215	220	225
His	Pro	Gly	Pro	Val	Asn	Ser	Glu	Leu	Phe	Leu	Arg	His	Val	Pro	230	235	240
Gly	Trp	Leu	Arg	Pro	Leu	Leu	Arg	Pro	Leu	Ala	Trp	Leu	Val	Leu	245	250	255
Arg	Ala	Pro	Arg	Gly	Gly	Ala	Gln	Thr	Pro	Leu	Tyr	Cys	Ala	Leu	260	265	270
Gln	Glu	Gly	Ile	Glu	Pro	Leu	Ser	Gly	Arg	Tyr	Phe	Ala	Asn	Cys	275	280	285
His	Val	Glu	Glu	Val	Pro	Pro	Ala	Ala	Arg	Asp	Asp	Arg	Ala	Ala	290	295	300
His	Arg	Leu	Trp	Glu	Ala	Ser	Lys	Arg	Leu	Ala	Gly	Leu	Gly	Pro	305	310	315
Gly	Glu	Asp	Ala	Glu	Pro	Asp	Glu	Asp	Pro	Gln	Ser	Glu	Asp	Ser	320	325	330
Glu	Ala	Pro	Ser	Ser	Leu	Ser	Thr	Pro	His	Pro	Glu	Glu	Pro	Thr	335	340	345
Val	Ser	Gln	Pro	Tyr	Pro	Ser	Pro	Gln	Ser	Ser	Pro	Asp	Leu	Ser	350	355	360

Lys Met Thr His Arg Ile Gln Ala Lys Val Glu Pro Glu Ile Gln
365 370 375

Leu Ser

<210> 207

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 207

cttcatggcc ttggacttgg ccag 24

<210> 208

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 208

acgccagtgg cctcaagctg gttg 24

<210> 209

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 209

ctttctgagc tctgagccac ggttggacat cctcatccac aatgc 45

<210> 210

<211> 3716

<212> DNA

<213> Homo sapiens

<400> 210

ggaggagaca gcctcctggg gggcaggggt tccctgctc tgctgctcct 50

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acccccagga ccagctgttc cagggccctg gccctgccag gatgagctgc 150

caagcctcag gccagccacc tcccaccatc cgctggttgc tgaatgggca 200

gcccctgagc atggtgcccc cagaccaca ccacctcctg cctgatggga 250

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 cttaagaaat ttgataccat aaaatggtaa aaaaaaaaaa aaaaaaaaaa 3700
 aaaaaaaaaa aaaaaa 3716

<210> 211
 <211> 985
 <212> PRT
 <213> Homo sapiens

<400> 211
 Met Gly Gly Met Ala Gln Asp Ser Pro Pro Gln Ile Leu Val His
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 Pro Gln Asp Gln Leu Phe Gln Gly Pro Gly Pro Ala Arg Met Ser
 20 25 30
 Cys Gln Ala Ser Gly Gln Pro Pro Pro Thr Ile Arg Trp Leu Leu
 35 40 45
 Asn Gly Gln Pro Leu Ser Met Val Pro Pro Asp Pro His His Leu
 50 55 60
 Leu Pro Asp Gly Thr Leu Leu Leu Leu Gln Pro Pro Ala Arg Gly
 65 70 75
 His Ala His Asp Gly Gln Ala Leu Ser Thr Asp Leu Gly Val Tyr
 80 85 90
 Thr Cys Glu Ala Ser Asn Arg Leu Gly Thr Ala Val Ser Arg Gly
 95 100 105
 Ala Arg Leu Ser Val Ala Val Leu Arg Glu Asp Phe Gln Ile Gln
 110 115 120
 Pro Arg Asp Met Val Ala Val Val Gly Glu Gln Phe Thr Leu Glu
 125 130 135

Cys Gly Pro Pro	Trp Gly His Pro Glu Pro Thr Val Ser Trp Trp	140	145	150
Lys Asp Gly Lys	Pro Leu Ala Leu Gln Pro Gly Arg His Thr Val	155	160	165
Ser Gly Gly Ser	Leu Leu Met Ala Arg Ala Glu Lys Ser Asp Glu	170	175	180
Gly Thr Tyr Met	Cys Val Ala Thr Asn Ser Ala Gly His Arg Glu	185	190	195
Ser Arg Ala Ala	Arg Val Ser Ile Gln Glu Pro Gln Asp Tyr Thr	200	205	210
Glu Pro Val Glu	Leu Leu Ala Val Arg Ile Gln Leu Glu Asn Val	215	220	225
Thr Leu Leu Asn	Pro Asp Pro Ala Glu Gly Pro Lys Pro Arg Pro	230	235	240
Ala Val Trp Leu	Ser Trp Lys Val Ser Gly Pro Ala Ala Pro Ala	245	250	255
Gln Ser Tyr Thr	Ala Leu Phe Arg Thr Gln Thr Ala Pro Gly Gly	260	265	270
Gln Gly Ala Pro	Trp Ala Glu Glu Leu Leu Ala Gly Trp Gln Ser	275	280	285
Ala Glu Leu Gly	Gly Leu His Trp Gly Gln Asp Tyr Glu Phe Lys	290	295	300
Val Arg Pro Ser	Ser Gly Arg Ala Arg Gly Pro Asp Ser Asn Val	305	310	315
Leu Leu Leu Arg	Leu Pro Glu Lys Val Pro Ser Ala Pro Pro Gln	320	325	330
Glu Val Thr Leu	Lys Pro Gly Asn Gly Thr Val Phe Val Ser Trp	335	340	345
Val Pro Pro Pro	Ala Glu Asn His Asn Gly Ile Ile Arg Gly Tyr	350	355	360
Gln Val Trp Ser	Leu Gly Asn Thr Ser Leu Pro Pro Ala Asn Trp	365	370	375
Thr Val Val Gly	Glu Gln Thr Gln Leu Glu Ile Ala Thr His Met	380	385	390
Pro Gly Ser Tyr	Cys Val Gln Val Ala Ala Val Thr Gly Ala Gly	395	400	405
Ala Gly Glu Pro	Ser Arg Pro Val Cys Leu Leu Leu Glu Gln Ala	410	415	420

Met	Glu	Arg	Ala	Thr	Gln	Glu	Pro	Ser	Glu	His	Gly	Pro	Trp	Thr				425	430	435
Leu	Glu	Gln	Leu	Arg	Ala	Thr	Leu	Lys	Arg	Pro	Glu	Val	Ile	Ala				440	445	450
Thr	Cys	Gly	Val	Ala	Leu	Trp	Leu	Leu	Leu	Leu	Gly	Thr	Ala	Val				455	460	465
Cys	Ile	His	Arg	Arg	Arg	Arg	Ala	Arg	Val	His	Leu	Gly	Pro	Gly				470	475	480
Leu	Tyr	Arg	Tyr	Thr	Ser	Glu	Asp	Ala	Ile	Leu	Lys	His	Arg	Met				485	490	495
Asp	His	Ser	Asp	Ser	Gln	Trp	Leu	Ala	Asp	Thr	Trp	Arg	Ser	Thr				500	505	510
Ser	Gly	Ser	Arg	Asp	Leu	Ser	Ser	Ser	Ser	Ser	Leu	Ser	Ser	Arg				515	520	525
Leu	Gly	Ala	Asp	Ala	Arg	Asp	Pro	Leu	Asp	Cys	Arg	Arg	Ser	Leu				530	535	540
Leu	Ser	Trp	Asp	Ser	Arg	Ser	Pro	Gly	Val	Pro	Leu	Leu	Pro	Asp				545	550	555
Thr	Ser	Thr	Phe	Tyr	Gly	Ser	Leu	Ile	Ala	Glu	Leu	Pro	Ser	Ser				560	565	570
Thr	Pro	Ala	Arg	Pro	Ser	Pro	Gln	Val	Pro	Ala	Val	Arg	Arg	Leu				575	580	585
Pro	Pro	Gln	Leu	Ala	Gln	Leu	Ser	Ser	Pro	Cys	Ser	Ser	Ser	Asp				590	595	600
Ser	Leu	Cys	Ser	Arg	Arg	Gly	Leu	Ser	Ser	Pro	Arg	Leu	Ser	Leu				605	610	615
Ala	Pro	Ala	Glu	Ala	Trp	Lys	Ala	Lys	Lys	Lys	Gln	Glu	Leu	Gln				620	625	630
His	Ala	Asn	Ser	Ser	Pro	Leu	Leu	Arg	Gly	Ser	His	Ser	Leu	Glu				635	640	645
Leu	Arg	Ala	Cys	Glu	Leu	Gly	Asn	Arg	Gly	Ser	Lys	Asn	Leu	Ser				650	655	660
Gln	Ser	Pro	Gly	Ala	Val	Pro	Gln	Ala	Leu	Val	Ala	Trp	Arg	Ala				665	670	675
Leu	Gly	Pro	Lys	Leu	Leu	Ser	Ser	Ser	Asn	Glu	Leu	Val	Thr	Arg				680	685	690
His	Leu	Pro	Pro	Ala	Pro	Leu	Phe	Pro	His	Glu	Thr	Pro	Pro	Thr				695	700	705

Gln Ser Gln Gln Thr Gln Pro Pro Val Ala Pro Gln Ala Pro Ser	710	715	720
Ser Ile Leu Leu Pro Ala Ala Pro Ile Pro Ile Leu Ser Pro Cys	725	730	735
Ser Pro Pro Ser Pro Gln Ala Ser Ser Leu Ser Gly Pro Ser Pro	740	745	750
Ala Ser Ser Arg Leu Ser Ser Ser Ser Leu Ser Ser Leu Gly Glu	755	760	765
Asp Gln Asp Ser Val Leu Thr Pro Glu Glu Val Ala Leu Cys Leu	770	775	780
Glu Leu Ser Glu Gly Glu Glu Thr Pro Arg Asn Ser Val Ser Pro	785	790	795
Met Pro Arg Ala Pro Ser Pro Pro Thr Thr Tyr Gly Tyr Ile Ser	800	805	810
Val Pro Thr Ala Ser Glu Phe Thr Asp Met Gly Arg Thr Gly Gly	815	820	825
Gly Val Gly Pro Lys Gly Gly Val Leu Leu Cys Pro Pro Arg Pro	830	835	840
Cys Leu Thr Pro Thr Pro Ser Glu Gly Ser Leu Ala Asn Gly Trp	845	850	855
Gly Ser Ala Ser Glu Asp Asn Ala Ala Ser Ala Arg Ala Ser Leu	860	865	870
Val Ser Ser Ser Asp Gly Ser Phe Leu Ala Asp Ala His Phe Ala	875	880	885
Arg Ala Leu Ala Val Ala Val Asp Ser Phe Gly Phe Gly Leu Glu	890	895	900
Pro Arg Glu Ala Asp Cys Val Phe Ile Asp Ala Ser Ser Pro Pro	905	910	915
Ser Pro Arg Asp Glu Ile Phe Leu Thr Pro Asn Leu Ser Leu Pro	920	925	930
Leu Trp Glu Trp Arg Pro Asp Trp Leu Glu Asp Met Glu Val Ser	935	940	945
His Thr Gln Arg Leu Gly Arg Gly Met Pro Pro Trp Pro Pro Asp	950	955	960
Ser Gln Ile Ser Ser Gln Arg Ser Gln Leu His Cys Arg Met Pro	965	970	975
Lys Ala Gly Ala Ser Pro Val Asp Tyr Ser	980	985	

<210> 212
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 212
gaaggacct acatgtgtgt ggcc 24

<210> 213
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 213
actgaccttc cagctgagcc acac 24

<210> 214
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 214
aggactacac ggagcctgtg gagcttctgg ctgtgcgaat tcagctggaa 50

<210> 215
<211> 2749
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1869, 1887
<223> unknown base

<400> 215
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gcgggttcga aggggacact gtgtccctgc agtgcaccta cagggaagag 150
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tcgctgctct ggcaccatct atgcagaaga agaaggccag gagacaatga 250
agggcaggggt gtccatccgt gacagccgcc aggagctctc gctcattgtg 300

accctgtgga acctcaccct gcaagacgct ggggagtact ggtgtggggt 350
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<210> 216

<211> 332

<212> PRT

<213> Homo sapiens

<400> 216

Met	Arg	Leu	Leu	Val	Leu	Leu	Trp	Gly	Cys	Leu	Leu	Leu	Pro	Gly
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Tyr	Glu	Ala	Leu	Glu	Gly	Pro	Glu	Glu	Ile	Ser	Gly	Phe	Glu	Gly
			20						25				30	

Asp	Thr	Val	Ser	Leu	Gln	Cys	Thr	Tyr	Arg	Glu	Glu	Leu	Arg	Asp
				35					40				45	

His	Arg	Lys	Tyr	Trp	Cys	Arg	Lys	Gly	Gly	Ile	Leu	Phe	Ser	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

				50						55					60
Cys	Ser	Gly	Thr	Ile	Tyr	Ala	Glu	Glu	Glu	Gly	Gln	Glu	Thr	Met	
				65						70				75	
Lys	Gly	Arg	Val	Ser	Ile	Arg	Asp	Ser	Arg	Gln	Glu	Leu	Ser	Leu	
				80					85					90	
Ile	Val	Thr	Leu	Trp	Asn	Leu	Thr	Leu	Gln	Asp	Ala	Gly	Glu	Tyr	
				95					100					105	
Trp	Cys	Gly	Val	Glu	Lys	Arg	Gly	Pro	Asp	Glu	Ser	Leu	Leu	Ile	
				110					115					120	
Ser	Leu	Phe	Val	Phe	Pro	Gly	Pro	Cys	Cys	Pro	Pro	Ser	Pro	Ser	
				125					130					135	
Pro	Thr	Phe	Gln	Pro	Leu	Ala	Thr	Thr	Arg	Leu	Gln	Pro	Lys	Ala	
				140					145					150	
Lys	Ala	Gln	Gln	Thr	Gln	Pro	Pro	Gly	Leu	Thr	Ser	Pro	Gly	Leu	
				155					160					165	
Tyr	Pro	Ala	Ala	Thr	Thr	Ala	Lys	Gln	Gly	Lys	Thr	Gly	Ala	Glu	
				170					175					180	
Ala	Pro	Pro	Leu	Pro	Gly	Thr	Ser	Gln	Tyr	Gly	His	Glu	Arg	Thr	
				185					190					195	
Ser	Gln	Tyr	Thr	Gly	Thr	Ser	Pro	His	Pro	Ala	Thr	Ser	Pro	Pro	
				200					205					210	
Ala	Gly	Ser	Ser	Arg	Pro	Pro	Met	Gln	Leu	Asp	Ser	Thr	Ser	Ala	
				215					220					225	
Glu	Asp	Thr	Ser	Pro	Ala	Leu	Ser	Ser	Gly	Ser	Ser	Lys	Pro	Arg	
				230					235					240	
Val	Ser	Ile	Pro	Met	Val	Arg	Ile	Leu	Ala	Pro	Val	Leu	Val	Leu	
				245					250					255	
Leu	Ser	Leu	Leu	Ser	Ala	Ala	Gly	Leu	Ile	Ala	Phe	Cys	Ser	His	
				260					265					270	
Leu	Leu	Leu	Trp	Arg	Lys	Glu	Ala	Gln	Gln	Ala	Thr	Glu	Thr	Gln	
				275					280					285	
Arg	Asn	Glu	Lys	Phe	Trp	Leu	Ser	Arg	Leu	Thr	Ala	Glu	Glu	Lys	
				290					295					300	
Glu	Ala	Pro	Ser	Gln	Ala	Pro	Glu	Gly	Asp	Val	Ile	Ser	Met	Pro	
				305					310					315	
Pro	Leu	His	Thr	Ser	Glu	Glu	Glu	Leu	Gly	Phe	Ser	Lys	Phe	Val	
				320					325					330	

Ser Ala

<210> 217
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 217
ccctgcagtg cacctacagg gaag 24

<210> 218
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 218
ctgtcttccc ctgcttggct gtgg 24

<210> 219
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 219
ggcgcaggaa ggggtgggac ctcttctctc gctgctctgg ccacatc 47

<210> 220
<211> 950
<212> DNA
<213> Homo sapiens

<400> 220
ttgtgactaa aagctggcct agcaggccag ggagtgcagc tgcaggcgtg 50
gggggtggcag gagccgcaga gccagagcag acagccgaga aacaggtgga 100
cagtgtgaaa gaaccagtgg tctcgctctg ttgccaggc tagagtgtac 150
tggcgtgata atagctcact gcagcctcag actcctggac ttgagaaatc 200
ctcctgcctt agcctcctgc atatctggga ctccaggggt gcactcaagc 250
cctgtttctt ctcttctgt gagtggacca cggaggctgg tgagctgcct 300
gtcatcccaa agctcagctc tgagccagag tgggtggtggc tccacctctg 350
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gctgggatca tgttgttggc cctggtctgt ctgctcagct gcctgctacc 450
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 atgacttcgg gctggacgga taccggggat acagcctggc tgactgggtc 550
 tgccttgctt atttcacaag cggtttcaac gcagctgctt tggactacga 600
 ggctgatggg agcaccaaca acgggatctt ccagatcaac agccggaggt 650
 ggtgcagcaa cctcaccctg aacgtcccca acgtgtgccg gatgtactgc 700
 tcagatttgt tgaatcctaa tctcaaggat accgttatct gtgccatgaa 750
 gataacccaa gagcctcagg gtctgggtta ctgggaggcc tggaggcatc 800
 actgccaggg aaaagacctc actgaatggg tggatggctg tgacttctag 850
 gatggacgga accatgcaca gcaggctggg aaatgtgggt tggttcctga 900
 cctaggcttg ggaagacaag ccagcgaata aaggatgggt gaacgtgaaa 950

<210> 221

<211> 146

<212> PRT

<213> Homo sapiens

<400> 221

Met	Leu	Leu	Ala	Leu	Val	Cys	Leu	Leu	Ser	Cys	Leu	Leu	Pro	Ser
1				5					10					15

Ser	Glu	Ala	Lys	Leu	Tyr	Gly	Arg	Cys	Glu	Leu	Ala	Arg	Val	Leu
				20					25					30

His	Asp	Phe	Gly	Leu	Asp	Gly	Tyr	Arg	Gly	Tyr	Ser	Leu	Ala	Asp
				35					40					45

Trp	Val	Cys	Leu	Ala	Tyr	Phe	Thr	Ser	Gly	Phe	Asn	Ala	Ala	Ala
				50					55					60

Leu	Asp	Tyr	Glu	Ala	Asp	Gly	Ser	Thr	Asn	Asn	Gly	Ile	Phe	Gln
				65					70					75

Ile	Asn	Ser	Arg	Arg	Trp	Cys	Ser	Asn	Leu	Thr	Pro	Asn	Val	Pro
				80					85					90

Asn	Val	Cys	Arg	Met	Tyr	Cys	Ser	Asp	Leu	Leu	Asn	Pro	Asn	Leu
				95					100					105

Lys	Asp	Thr	Val	Ile	Cys	Ala	Met	Lys	Ile	Thr	Gln	Glu	Pro	Gln
				110					115					120

Gly	Leu	Gly	Tyr	Trp	Glu	Ala	Trp	Arg	His	His	Cys	Gln	Gly	Lys
				125					130					135

Asp	Leu	Thr	Glu	Trp	Val	Asp	Gly	Cys	Asp	Phe
				140					145	

<210> 222
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 222
gggatcatgt tggtggcct ggtc 24

<210> 223
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 223
gcaaggcaga cccagtcagc cag 23

<210> 224
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 224
ctgcctgcta ccctccaagt gaggccaagc tctacggtcg ttgtg 45

<210> 225
<211> 2049
<212> DNA
<213> Homo sapiens

<400> 225
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cgagcaactg gctgtacctg gccaaactgt cgtcgggtggg gagcatctca 150
gaggaggaga cgtgcgagaa actcaagggc ctgatccaga ggcagggtgca 200
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tgctccacac tcgactcctt gcccgcttcc ggcaagggtg tgacgcaagg 350
gactcgggag gcggccttcg tgtacgcat ctcttcggca ggtgtggcct 400
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gacaggacag tgcattgggt cagcccacag ggcttccagt ggtcaggatg 500
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gagccgtgcc gcccttccgc cagggtgggtc acgcactgaa ggagaagttt 750
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acacacacac ggacacacac acacacctgc gagagagagg gaggaaggg 2000
ctgtgccttt gcagtcacgc ccgagtcacc tttcacagca ctgttcctc 2049

<210> 226
<211> 351
<212> PRT
<213> Homo sapiens

<400> 226

Met	Ser	Pro	Arg	Ser	Cys	Leu	Arg	Ser	Leu	Arg	Leu	Leu	Val	Phe	1	5	10	15
Ala	Val	Phe	Ser	Ala	Ala	Ala	Ser	Asn	Trp	Leu	Tyr	Leu	Ala	Lys	20	25	30	
Leu	Ser	Ser	Val	Gly	Ser	Ile	Ser	Glu	Glu	Glu	Thr	Cys	Glu	Lys	35	40	45	
Leu	Lys	Gly	Leu	Ile	Gln	Arg	Gln	Val	Gln	Met	Cys	Lys	Arg	Asn	50	55	60	
Leu	Glu	Val	Met	Asp	Ser	Val	Arg	Arg	Gly	Ala	Gln	Leu	Ala	Ile	65	70	75	
Glu	Glu	Cys	Gln	Tyr	Gln	Phe	Arg	Asn	Arg	Arg	Trp	Asn	Cys	Ser	80	85	90	
Thr	Leu	Asp	Ser	Leu	Pro	Val	Phe	Gly	Lys	Val	Val	Thr	Gln	Gly	95	100	105	
Thr	Arg	Glu	Ala	Ala	Phe	Val	Tyr	Ala	Ile	Ser	Ser	Ala	Gly	Val	110	115	120	
Ala	Phe	Ala	Val	Thr	Arg	Ala	Cys	Ser	Ser	Gly	Glu	Leu	Glu	Lys	125	130	135	
Cys	Gly	Cys	Asp	Arg	Thr	Val	His	Gly	Val	Ser	Pro	Gln	Gly	Phe	140	145	150	
Gln	Trp	Ser	Gly	Cys	Ser	Asp	Asn	Ile	Ala	Tyr	Gly	Val	Ala	Phe	155	160	165	
Ser	Gln	Ser	Phe	Val	Asp	Val	Arg	Glu	Arg	Ser	Lys	Gly	Ala	Ser	170	175	180	
Ser	Ser	Arg	Ala	Leu	Met	Asn	Leu	His	Asn	Asn	Glu	Ala	Gly	Arg	185	190	195	
Lys	Ala	Ile	Leu	Thr	His	Met	Arg	Val	Glu	Cys	Lys	Cys	His	Gly	200	205	210	
Val	Ser	Gly	Ser	Cys	Glu	Val	Lys	Thr	Cys	Trp	Arg	Ala	Val	Pro				

215	220	225
Pro Phe Arg Gln Val Gly His Ala Leu Lys Glu Lys Phe Asp Gly		
230	235	240
Ala Thr Glu Val Glu Pro Arg Arg Val Gly Ser Ser Arg Ala Leu		
245	250	255
Val Pro Arg Asn Ala Gln Phe Lys Pro His Thr Asp Glu Asp Leu		
260	265	270
Val Tyr Leu Glu Pro Ser Pro Asp Phe Cys Glu Gln Asp Met Arg		
275	280	285
Ser Gly Val Leu Gly Thr Arg Gly Arg Thr Cys Asn Lys Thr Ser		
290	295	300
Lys Ala Ile Asp Gly Cys Glu Leu Leu Cys Cys Gly Arg Gly Phe		
305	310	315
His Thr Ala Gln Val Glu Leu Ala Glu Arg Cys Ser Cys Lys Phe		
320	325	330
His Trp Cys Cys Phe Val Lys Cys Arg Gln Cys Gln Arg Leu Val		
335	340	345
Glu Leu His Thr Cys Arg		
350		

<210> 227

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 227

gctgcagctg caaattccac tgg 23

<210> 228

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 228

tggtgggaga ctgtttaa at t atcggcc 28

<210> 229

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 229

tgcttcgtca agtgccggca gtgccagcgg ctctgtggagt t 41

<210> 230

<211> 1355

<212> DNA

<213> Homo sapiens

<400> 230

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gctccgagga ggtccccgga gggccctggg gacgctgggt gcactggagc 150
aggagacccc tcttcttggc cctggctgtc ctggtcacca cagtcctttg 200
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agaactgtgt catgatgctg cacacggggc tgtggaacga cgcaccgtgt 900
gacagcgaga aggacggctg gatctgtgag aaaaggcaca actgctgacc 950
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 aaaaa 1355

<210> 231
 <211> 293
 <212> PRT
 <213> Homo sapiens

<400> 231

Met	Asp	Thr	Thr	Arg	Tyr	Ser	Lys	Trp	Gly	Gly	Ser	Ser	Glu	Glu	1	5	10	15
Val	Pro	Gly	Gly	Pro	Trp	Gly	Arg	Trp	Val	His	Trp	Ser	Arg	Arg	20	25	30	
Pro	Leu	Phe	Leu	Ala	Leu	Ala	Val	Leu	Val	Thr	Thr	Val	Leu	Trp	35	40	45	
Ala	Val	Ile	Leu	Ser	Ile	Leu	Leu	Ser	Lys	Ala	Ser	Thr	Glu	Arg	50	55	60	
Ala	Ala	Leu	Leu	Asp	Gly	His	Asp	Leu	Leu	Arg	Thr	Asn	Ala	Ser	65	70	75	
Lys	Gln	Thr	Ala	Ala	Leu	Gly	Ala	Leu	Lys	Glu	Glu	Val	Gly	Asp	80	85	90	
Cys	His	Ser	Cys	Cys	Ser	Gly	Thr	Gln	Ala	Gln	Leu	Gln	Thr	Thr	95	100	105	
Arg	Ala	Glu	Leu	Gly	Glu	Ala	Gln	Ala	Lys	Leu	Met	Glu	Gln	Glu	110	115	120	
Ser	Ala	Leu	Arg	Glu	Leu	Arg	Glu	Arg	Val	Thr	Gln	Gly	Leu	Ala	125	130	135	
Glu	Ala	Gly	Arg	Gly	Arg	Glu	Asp	Val	Arg	Thr	Glu	Leu	Phe	Arg	140	145	150	
Ala	Leu	Glu	Ala	Val	Arg	Leu	Gln	Asn	Asn	Ser	Cys	Glu	Pro	Cys	155	160	165	
Pro	Thr	Ser	Trp	Leu	Ser	Phe	Glu	Gly	Ser	Cys	Tyr	Phe	Phe	Ser	170	175	180	
Val	Pro	Lys	Thr	Thr	Trp	Ala	Ala	Ala	Gln	Asp	His	Cys	Ala	Asp	185	190	195	
Ala	Ser	Ala	His	Leu	Val	Ile	Val	Gly	Gly	Leu	Asp	Glu	Gln	Gly	200	205	210	

Phe	Leu	Thr	Arg	Asn	Thr	Arg	Gly	Arg	Gly	Tyr	Trp	Leu	Gly	Leu	215	220	225
Arg	Ala	Val	Arg	His	Leu	Gly	Lys	Val	Gln	Gly	Tyr	Gln	Trp	Val	230	235	240
Asp	Gly	Val	Ser	Leu	Ser	Phe	Ser	His	Trp	Asn	Gln	Gly	Glu	Pro	245	250	255
Asn	Asp	Ala	Trp	Gly	Arg	Glu	Asn	Cys	Val	Met	Met	Leu	His	Thr	260	265	270
Gly	Leu	Trp	Asn	Asp	Ala	Pro	Cys	Asp	Ser	Glu	Lys	Asp	Gly	Trp	275	280	285
Ile	Cys	Glu	Lys	Arg	His	Asn	Cys								290		

<210> 232

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

gcgagaactg tgatcatgatg ctgc 24

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 233

gtttctgaga ctcagcagcg gtgg 24

<210> 234

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 234

caccgtgtga cagcgagaag gacggctgga tctgtgagaa aaggcacaac 50

<210> 235

<211> 1847

<212> DNA

<213> Homo sapiens

<400> 235

gccaggggaa gaggggtgatc cgacccgggg aaggtcgctg ggcagggcga 50
gttgggaaag cggcagcccc cgccgcccc gcagcccctt ctctccttt 100
ctcccacgtc ctatctgcct ctcgctggag gccaggccgt gcagcatcga 150
agacaggagg aactggagcc tcattggccg gcccggggcg ccggcctcgg 200
gcttaaatag gagctccggg ctctggctgg gacccgaccg ctgccggccg 250
cgctcccgt gctcctgccg ggtgatggaa aaccccagcc cggccgccgc 300
cctgggcaag gccctctgcg ctctcctcct ggccactctc ggcgccgccg 350
gccagcctct tgggggagag tccatctgtt ccgccagagc cccggccaaa 400
tacagcatca ccttcacggg caagtggagc cagacggcct tccccagca 450
gtaccccctg ttccgcccc ctgcgcagtg gtcttcgctg ctgggggccg 500
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actaccgcg gctgaaggcc ctgcctccca tcgccagggt gacactgctg 1000
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cagcagggac aatgagattg tagacagcg ctcagttcca gaaacgccgc 1100
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cgccaacaac gggagcccct gccccgagct cgaagaagag gctgagtgcg 1250
tccttgataa ctgcgtctaa gaccagagcc ccgcagcccc tggggcccc 1300
cggagccatg ggggtgcggg ggctcctgtg caggctcatg ctgcaggcgg 1350
ccgagggcac agggggtttc gcgctgctcc tgaccgcggt gaggccgcgc 1400

cgaccatctc tgcactgaag ggccctctgg tggccggcac gggcattggg 1450
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 gtctgtcttc agcctcctcc tctgcagga taaagtcac cccaaggctc 1550
 cagctactct aaattatgtc tccttataag ttattgtctgc tccaggagat 1600
 tgtccttcat cgtccagggg cctgggtccc acgtggttgc agatacctca 1650
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 agcggggggcc acttgagaag tgaataaatg gggcggtttc ggaagcgtca 1750
 gtgtttccat gttatggatc tctctgcgtt tgaataaaga ctatctctgt 1800
 tgctcacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1847

<210> 236
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 236

Met	Glu	Asn	Pro	Ser	Pro	Ala	Ala	Ala	Leu	Gly	Lys	Ala	Leu	Cys
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Ala	Leu	Leu	Leu	Ala	Thr	Leu	Gly	Ala	Ala	Gly	Gln	Pro	Leu	Gly
				20					25					30
Gly	Glu	Ser	Ile	Cys	Ser	Ala	Arg	Ala	Pro	Ala	Lys	Tyr	Ser	Ile
				35					40					45
Thr	Phe	Thr	Gly	Lys	Trp	Ser	Gln	Thr	Ala	Phe	Pro	Lys	Gln	Tyr
				50					55					60
Pro	Leu	Phe	Arg	Pro	Pro	Ala	Gln	Trp	Ser	Ser	Leu	Leu	Gly	Ala
				65					70					75
Ala	His	Ser	Ser	Asp	Tyr	Ser	Met	Trp	Arg	Lys	Asn	Gln	Tyr	Val
				80					85					90
Ser	Asn	Gly	Leu	Arg	Asp	Phe	Ala	Glu	Arg	Gly	Glu	Ala	Trp	Ala
				95					100					105
Leu	Met	Lys	Glu	Ile	Glu	Ala	Ala	Gly	Glu	Ala	Leu	Gln	Ser	Val
				110					115					120
His	Glu	Val	Phe	Ser	Ala	Pro	Ala	Val	Pro	Ser	Gly	Thr	Gly	Gln
				125					130					135
Thr	Ser	Ala	Glu	Leu	Glu	Val	Gln	Arg	Arg	His	Ser	Leu	Val	Ser
				140					145					150
Phe	Val	Val	Arg	Ile	Val	Pro	Ser	Pro	Asp	Trp	Phe	Val	Gly	Val
				155					160					165

Asp Ser Leu Asp Leu Cys Asp Gly Asp Arg Trp Arg Glu Gln Ala		
	170	180
Ala Leu Asp Leu Tyr Pro Tyr Asp Ala Gly Thr Asp Ser Gly Phe		
	185	195
Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp Thr Val		
	200	210
Thr Glu Ile Thr Ser Ser Ser Pro Ser His Pro Ala Asn Ser Phe		
	215	225
Tyr Tyr Pro Arg Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr		
	230	240
Leu Leu Arg Leu Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala		
	245	255
Pro Val Leu Pro Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser		
	260	270
Val Pro Glu Thr Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser		
	275	285
Trp Gly Leu Cys Gly Gly His Cys Gly Arg Leu Gly Thr Lys Ser		
	290	300
Arg Thr Arg Tyr Val Arg Val Gln Pro Ala Asn Asn Gly Ser Pro		
	305	315
Cys Pro Glu Leu Glu Glu Glu Ala Glu Cys Val Pro Asp Asn Cys		
	320	330

Val

<210> 237

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

cagcactgcc aggggaagag gg 22

<210> 238

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 238

caggactcgc tacgtccg 18

<210> 239
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 239
cagccccttc tcctcctttc tccc 24

<210> 240
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 240
gcagttatca gggacgcact cagcc 25

<210> 241
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 241
ccagcgagag gcagatag 18

<210> 242
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 242
cggtcaccgt gtcctgcggg atg 23

<210> 243
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 243
cagccccttc tcctcctttc tcccacgtcc tatctgcctc tc 42

<210> 244

<211> 1894
<212> DNA
<213> Homo sapiens

<400> 244
ggcggcgtcc gtgaggggct cctttgggca ggggtagtgt ttggtgtccc 50
tgtcttgctg gatattgaca aactgaagct ttcttgacc actggactta 100
aggaagagtg tactcgtagg cggacagctt tagtgccgg ccggccgctc 150
tcatcccccg taaggagcag agtcctttgt actgaccaag atgagcaaca 200
tctacatcca ggagcctccc acgaatggga aggttttatt gaaaactaca 250
gctggagata ttgacataga gttgtggtcc aaagaagctc ctaaagcttg 300
cagaaatfff atccaactff gtttggagc ttattatgac aataccatff 350
ttcatagagt tgtgcctggt ttcatagtcc aaggcggaga tcctactggc 400
acagggagtg gtggagagtc tatctatgga gcgccattca aagatgaatt 450
tcattcacgg ttgcgtttta atcggagagg actggttgcc atggcaaatg 500
ctggtttctca tgataatggc agccagtttt tcttcacact gggtcgagca 550
gatgaactta acaataagca taccatcttt ggaaagggtta caggggatac 600
agtatataac atgttgcgac tgtcagaagt agacattgat gatgacgaaa 650
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aagtggagaa gaaatcagtc agccgcagtg aagagctcag aaaagaagca 1150
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tgcagcaaaa caagcagaaa aaagaagtga agaggaagaa gcccctccag 1250
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 ctgaaaatga cattcctgaa acagaagtag aagatgatga aggatggatg 1450
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 catgcaagac tcagatacat ttgaaatcta tgatcctcgg aatccagtga 1550
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 agaagataaa atgagaataa tgataaccag aacttgctgg aaatgtgcct 1650
 acaatggcct tgtaacagcc attgttccca acagcatcac ttaggggtgt 1700
 gaaaagaagt atttttgaac ctgttgtctg gttttgaaaa acaattatct 1750
 tgttttgcaa attgtggaat gatgtaagca aatgcttttg gttactggta 1800
 catgtgtttt ttcctagctg accttttata ttgctaaatc tgaaataaaa 1850
 taactttcct tccacaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1894

<210> 245
 <211> 472
 <212> PRT
 <213> Homo sapiens

<400> 245
 Met Ser Asn Ile Tyr Ile Gln Glu Pro Pro Thr Asn Gly Lys Val
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 Leu Leu Lys Thr Thr Ala Gly Asp Ile Asp Ile Glu Leu Trp Ser
 20 25 30
 Lys Glu Ala Pro Lys Ala Cys Arg Asn Phe Ile Gln Leu Cys Leu
 35 40 45
 Glu Ala Tyr Tyr Asp Asn Thr Ile Phe His Arg Val Val Pro Gly
 50 55 60
 Phe Ile Val Gln Gly Gly Asp Pro Thr Gly Thr Gly Ser Gly Gly
 65 70 75
 Glu Ser Ile Tyr Gly Ala Pro Phe Lys Asp Glu Phe His Ser Arg
 80 85 90
 Leu Arg Phe Asn Arg Arg Gly Leu Val Ala Met Ala Asn Ala Gly
 95 100 105
 Ser His Asp Asn Gly Ser Gln Phe Phe Phe Thr Leu Gly Arg Ala
 110 115 120
 Asp Glu Leu Asn Asn Lys His Thr Ile Phe Gly Lys Val Thr Gly
 125 130 135

Asp Thr Val Tyr	Asn Met Leu Arg Leu Ser Glu Val Asp Ile Asp	140	145	150
Asp Asp Glu Arg	Pro His Asn Pro His Lys Ile Lys Ser Cys Glu	155	160	165
Val Leu Phe Asn	Pro Phe Asp Asp Ile Ile Pro Arg Glu Ile Lys	170	175	180
Arg Leu Lys Lys	Glu Lys Pro Glu Glu Glu Val Lys Lys Leu Lys	185	190	195
Pro Lys Gly Thr	Lys Asn Phe Ser Leu Leu Ser Phe Gly Glu Glu	200	205	210
Ala Glu Glu Glu	Glu Glu Glu Val Asn Arg Val Ser Gln Ser Met	215	220	225
Lys Gly Lys Ser	Lys Ser Ser His Asp Leu Leu Lys Asp Asp Pro	230	235	240
His Leu Ser Ser	Val Pro Val Val Glu Ser Glu Lys Gly Asp Ala	245	250	255
Pro Asp Leu Val	Asp Asp Gly Glu Asp Glu Ser Ala Glu His Asp	260	265	270
Glu Tyr Ile Asp	Gly Asp Glu Lys Asn Leu Met Arg Glu Arg Ile	275	280	285
Ala Lys Lys Leu	Lys Lys Asp Thr Ser Ala Asn Val Lys Ser Ala	290	295	300
Gly Glu Gly Glu	Val Glu Lys Lys Ser Val Ser Arg Ser Glu Glu	305	310	315
Leu Arg Lys Glu	Ala Arg Gln Leu Lys Arg Glu Leu Leu Ala Ala	320	325	330
Lys Gln Lys Lys	Val Glu Asn Ala Ala Lys Gln Ala Glu Lys Arg	335	340	345
Ser Glu Glu Glu	Glu Ala Pro Pro Asp Gly Ala Val Ala Glu Tyr	350	355	360
Arg Arg Glu Lys	Gln Lys Tyr Glu Ala Leu Arg Lys Gln Gln Ser	365	370	375
Lys Lys Gly Thr	Ser Arg Glu Asp Gln Thr Leu Ala Leu Leu Asn	380	385	390
Gln Phe Lys Ser	Lys Leu Thr Gln Ala Ile Ala Glu Thr Pro Glu	395	400	405
Asn Asp Ile Pro	Glu Thr Glu Val Glu Asp Asp Glu Gly Trp Met	410	415	420

Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg Lys Val Lys Asp
425 430 435

Ala Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr Asp Pro Arg
440 445 450

Asn Pro Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys Leu Met
455 460 465

Arg Glu Lys Lys Glu Arg Arg
470

<210> 246

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

tgcgagatc ctactggcac aggg 24

<210> 247

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 247

cgagttagtc agagcatg 18

<210> 248

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 248

cagatggtgc tgttgccg 18

<210> 249

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 249

caactggaac aggaactgag atgtggatc 29

<210> 250

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 250
ctggttcagc agtgcaaggg tctg 24

<210> 251
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 251
cctctccgat taaaacgc 18

<210> 252
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 252
gagaggactg gttgcatgg caaatgctgg ttctcatgat aatgg 45

<210> 253
<211> 2456
<212> DNA
<213> Homo sapiens

<400> 253
cgccgccgtt ggggctggaa gttcccgcca ggtccgtgcc gggcgagaga 50
gatgctgccc ggcccgcctc ggctttgagg cgagagaagt gtcccagacc 100
catttcgcct tgetgacggc gtcgagccct ggccagacat gtccacaggg 150
ttctccttcg ggtccgggac tctgggctcc accaccgtgg ccgccggcgg 200
gaccagcaca ggcggcgttt tctccttcgg aacgggaacg tctagcaacc 250
cttctgtggg gctcaatttt ggaaatcttg gaagtacttc aactccagca 300
actacatctg ctcccttcaag tggttttgga accgggctct ttggatctaa 350
acctgccact gggttcactc taggaggaac aaatacaggt gccttgca 400
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atgcatgtgg ggaagacacc catccaagtc tttttaggag tccccttctc 500

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catgagccct gtggtggatg gtgtggtgat cccagatgac cctttggtgc 1450
tcctgacca ggggaaggtt tcctctgtgc cctaccttct aggtgtcaac 1500
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accacttgtg gtggaggagt acctggacaa tgtcaatgag catgactgga 1600
agatgctacg aaaccgtatg atggacatag ttcaagatgc cactttcgtg 1650
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caggccctgg ggagactagc catggacata cctggggaca agagttctac 1950
 ccaccccaagt ttagaactgc aggagctccc tgctgcctcc aggccaaagc 2000
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 tggcctggag gcctagggca ggttgtgaca tggagcaaac ttttggtagt 2350
 ttgggatctt ctctcccacc cacacttatc tccccaggg cactccaaa 2400
 gtctatacac aggggtggtc tcttcaataa agaagtgttg attagaaaaa 2450
 aaaaaa 2456

<210> 254
 <211> 545
 <212> PRT
 <213> Homo sapiens

<400> 254
 Met Ser Thr Gly Phe Ser Phe Gly Ser Gly Thr Leu Gly Ser Thr
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 Thr Val Ala Ala Gly Gly Thr Ser Thr Gly Gly Val Phe Ser Phe
 20 25 30
 Gly Thr Gly Thr Ser Ser Asn Pro Ser Val Gly Leu Asn Phe Gly
 35 40 45
 Asn Leu Gly Ser Thr Ser Thr Pro Ala Thr Thr Ser Ala Pro Ser
 50 55 60
 Ser Gly Phe Gly Thr Gly Leu Phe Gly Ser Lys Pro Ala Thr Gly
 65 70 75
 Phe Thr Leu Gly Gly Thr Asn Thr Gly Ala Leu His Thr Lys Arg
 80 85 90
 Pro Gln Val Val Thr Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met
 95 100 105
 His Val Gly Lys Thr Pro Ile Gln Val Phe Leu Gly Val Pro Phe
 110 115 120
 Ser Arg Pro Pro Leu Gly Ile Leu Arg Phe Ala Pro Pro Glu Pro
 125 130 135

Pro Glu Pro Trp Lys Gly Ile Arg Asp Ala Thr Thr Tyr Pro Pro	140	145	150
Gly Trp Ser Leu Ala Leu Ser Pro Gly Trp Ser Ala Val Ala Arg	155	160	165
Ser Arg Leu Thr Ala Thr Ser Ala Ser Arg Val Gln Ala Ser Leu	170	175	180
Leu Pro Gln Pro Leu Ser Val Trp Gly Tyr Arg Cys Leu Gln Glu	185	190	195
Ser Trp Gly Gln Leu Ala Ser Met Tyr Val Ser Thr Arg Glu Arg	200	205	210
Tyr Lys Trp Leu Arg Phe Ser Glu Asp Cys Leu Tyr Leu Asn Val	215	220	225
Tyr Ala Pro Ala Arg Ala Pro Gly Asp Pro Gln Leu Pro Val Met	230	235	240
Val Trp Phe Pro Gly Gly Ala Phe Ile Val Gly Ala Ala Ser Ser	245	250	255
Tyr Glu Gly Ser Asp Leu Ala Ala Arg Glu Lys Val Val Leu Val	260	265	270
Phe Leu Gln His Arg Leu Gly Ile Phe Gly Phe Leu Ser Thr Asp	275	280	285
Asp Ser His Ala Arg Gly Asn Trp Gly Leu Leu Asp Gln Met Ala	290	295	300
Ala Leu Arg Trp Val Gln Glu Asn Ile Ala Ala Phe Gly Gly Asp	305	310	315
Pro Gly Asn Val Thr Leu Phe Gly Gln Ser Ala Gly Ala Met Ser	320	325	330
Ile Ser Gly Leu Met Met Ser Pro Leu Ala Ser Gly Leu Phe His	335	340	345
Arg Ala Ile Ser Gln Ser Gly Thr Ala Leu Phe Arg Leu Phe Ile	350	355	360
Thr Ser Asn Pro Leu Lys Val Ala Lys Lys Val Ala His Leu Ala	365	370	375
Gly Cys Asn His Asn Ser Thr Gln Ile Leu Val Asn Cys Leu Arg	380	385	390
Ala Leu Ser Gly Thr Lys Val Met Arg Val Ser Asn Lys Met Arg	395	400	405
Phe Leu Gln Leu Asn Phe Gln Arg Asp Pro Glu Glu Ile Ile Trp	410	415	420

Ser Met Ser Pro Val Val Asp Gly Val Val Ile Pro Asp Asp Pro	425	430	435
Leu Val Leu Leu Thr Gln Gly Lys Val Ser Ser Val Pro Tyr Leu	440	445	450
Leu Gly Val Asn Asn Leu Glu Phe Asn Trp Leu Leu Pro Tyr Asn	455	460	465
Ile Thr Lys Glu Gln Val Pro Leu Val Val Glu Glu Tyr Leu Asp	470	475	480
Asn Val Asn Glu His Asp Trp Lys Met Leu Arg Asn Arg Met Met	485	490	495
Asp Ile Val Gln Asp Ala Thr Phe Val Tyr Ala Thr Leu Gln Thr	500	505	510
Ala His Tyr His Arg Glu Thr Pro Met Met Gly Ile Cys Pro Ala	515	520	525
Gly His Ala Thr Thr Arg Met Lys Ser Thr Cys Ser Trp Ile Leu	530	535	540
Pro Gln Glu Trp Ala	545		

<210> 255

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 255

aggtgcctgc aggagtcctg ggg 23

<210> 256

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 256

ccacctcagg aagccgaaga tgcc 24

<210> 257

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 257

gaacgggtaca agtggctgcg cttcagcgag gactgtctgt acctg 45

<210> 258

<211> 2764

<212> DNA

<213> Homo sapiens

<400> 258

gagaacaggc ctgtctcagg caggccctgc gcctcctatg cggagatgct 50

actgccactg ctgctgtcct cgctgctggg cgggtcccag gctatggatg 100

ggagattctg gatacgagtg caggagtcag tgatggtgcc ggagggcctg 150

tgcattctctg tgccctgctc tttctcctac ccccgacaag actggacagg 200

gtctacccca gcttatggct actggttcaa agcagtgact gagacaacca 250

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<210> 259
 <211> 544
 <212> PRT
 <213> Homo sapiens

<400> 259

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Ala	Met	Asp	Gly	Arg	Phe	Trp	Ile	Arg	Val	Gln	Glu	Ser	Val	Met	20	25	30	
Val	Pro	Glu	Gly	Leu	Cys	Ile	Ser	Val	Pro	Cys	Ser	Phe	Ser	Tyr	35	40	45	
Pro	Arg	Gln	Asp	Trp	Thr	Gly	Ser	Thr	Pro	Ala	Tyr	Gly	Tyr	Trp	50	55	60	
Phe	Lys	Ala	Val	Thr	Glu	Thr	Thr	Lys	Gly	Ala	Pro	Val	Ala	Thr	65	70	75	
Asn	His	Gln	Ser	Arg	Glu	Val	Glu	Met	Ser	Thr	Arg	Gly	Arg	Phe	80	85	90	
Gln	Leu	Thr	Gly	Asp	Pro	Ala	Lys	Gly	Asn	Cys	Ser	Leu	Val	Ile	95	100	105	
Arg	Asp	Ala	Gln	Met	Gln	Asp	Glu	Ser	Gln	Tyr	Phe	Phe	Arg	Val	110	115	120	
Glu	Arg	Gly	Ser	Tyr	Val	Thr	Tyr	Asn	Phe	Met	Asn	Asp	Gly	Phe	125	130	135	
Phe	Leu	Lys	Val	Thr	Val	Leu	Ser	Phe	Thr	Pro	Arg	Pro	Gln	Asp	140	145	150	
His	Asn	Thr	Asp	Leu	Thr	Cys	His	Val	Asp	Phe	Ser	Arg	Lys	Gly	155	160	165	
Val	Ser	Ala	Gln	Arg	Thr	Val	Arg	Leu	Arg	Val	Ala	Tyr	Ala	Pro	170	175	180	
Arg	Asp	Leu	Val	Ile	Ser	Ile	Ser	Arg	Asp	Asn	Thr	Pro	Ala	Leu	185	190	195	
Glu	Pro	Gln	Pro	Gln	Gly	Asn	Val	Pro	Tyr	Leu	Glu	Ala	Gln	Lys	200	205	210	
Gln	Phe	Leu	Arg	Leu	Leu	Cys	Ala	Ala	Asp	Ser	Gln	Pro	Pro	215	220	225		

Ala Thr Leu Ser Trp Val Leu Gln Asn Arg Val Leu Ser Ser Ser	230	235	240
His Pro Trp Gly Pro Arg Pro Leu Gly Leu Glu Leu Pro Gly Val	245	250	255
Lys Ala Gly Asp Ser Gly Arg Tyr Thr Cys Arg Ala Glu Asn Arg	260	265	270
Leu Gly Ser Gln Gln Arg Ala Leu Asp Leu Ser Val Gln Tyr Pro	275	280	285
Pro Glu Asn Leu Arg Val Met Val Ser Gln Ala Asn Arg Thr Val	290	295	300
Leu Glu Asn Leu Gly Asn Gly Thr Ser Leu Pro Val Leu Glu Gly	305	310	315
Gln Ser Leu Cys Leu Val Cys Val Thr His Ser Ser Pro Pro Ala	320	325	330
Arg Leu Ser Trp Thr Gln Arg Gly Gln Val Leu Ser Pro Ser Gln	335	340	345
Pro Ser Asp Pro Gly Val Leu Glu Leu Pro Arg Val Gln Val Glu	350	355	360
His Glu Gly Glu Phe Thr Cys His Ala Arg His Pro Leu Gly Ser	365	370	375
Gln His Val Ser Leu Ser Leu Ser Val His Tyr Lys Lys Gly Leu	380	385	390
Ile Ser Thr Ala Phe Ser Asn Gly Ala Phe Leu Gly Ile Gly Ile	395	400	405
Thr Ala Leu Leu Phe Leu Cys Leu Ala Leu Ile Ile Met Lys Ile	410	415	420
Leu Pro Lys Arg Arg Thr Gln Thr Glu Thr Pro Arg Pro Arg Phe	425	430	435
Ser Arg His Ser Thr Ile Leu Asp Tyr Ile Asn Val Val Pro Thr	440	445	450
Ala Gly Pro Leu Ala Gln Lys Arg Asn Gln Lys Ala Thr Pro Asn	455	460	465
Ser Pro Arg Thr Pro Pro Pro Pro Gly Ala Pro Ser Pro Glu Ser	470	475	480
Lys Lys Asn Gln Lys Lys Gln Tyr Gln Leu Pro Ser Phe Pro Glu	485	490	495
Pro Lys Ser Ser Thr Gln Ala Pro Glu Ser Gln Glu Ser Gln Glu	500	505	510

Glu Leu His Tyr Ala Thr Leu Asn Phe Pro Gly Val Arg Pro Arg
515 520 525

Pro Glu Ala Arg Met Pro Lys Gly Thr Gln Ala Asp Tyr Ala Glu
530 535 540

Val Lys Phe Gln

<210> 260

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 260

caaagcctgc gcctgggtctg tg 22

<210> 261

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 261

ttctggagcc cagaggggtgc tgag 24

<210> 262

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 262

ggagctgccca cccattcaaaa tggagcacga aggagagttc acctg 45

<210> 263

<211> 2857

<212> DNA

<213> Homo sapiens

<400> 263

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actgctgcgt tttatgttgg gaattcctct cctatggcct tgtcttggag 100

caacagaaaa ctctcaaaca aagaaagtca agcagccagt gcgatctcat 150

ttgagagtga agcgtggcctg ggtgtggaac caattttttg taccagagga 200

aatgaatacg actagtcatc acatcggcca gctaagatct gatttagaca 250
atggaaacaa ttctttccag tacaagcttt tgggagctgg agctggaagt 300
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cattgtacca gagatgtctc cagaaggaac attagttatc caggtgacag 550
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 tatagtcaga gaaattttca tgaattattc catgaagtat tgtttccttt 2850
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<210> 264

<211> 772

<212> PRT

<213> Homo sapiens

<400> 264

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Leu	Trp	Pro	Cys	Leu	Gly	Ala	Thr	Glu	Asn	Ser	Gln	Thr	Lys	Lys		20	25		30
Val	Lys	Gln	Pro	Val	Arg	Ser	His	Leu	Arg	Val	Lys	Arg	Gly	Trp		35	40		45
Val	Trp	Asn	Gln	Phe	Phe	Val	Pro	Glu	Glu	Met	Asn	Thr	Thr	Ser		50	55		60
His	His	Ile	Gly	Gln	Leu	Arg	Ser	Asp	Leu	Asp	Asn	Gly	Asn	Asn		65	70		75
Ser	Phe	Gln	Tyr	Lys	Leu	Leu	Gly	Ala	Gly	Ala	Gly	Ser	Thr	Phe		80	85		90
Ile	Ile	Asp	Glu	Arg	Thr	Gly	Asp	Ile	Tyr	Ala	Ile	Gln	Lys	Leu		95	100		105
Asp	Arg	Glu	Glu	Arg	Ser	Leu	Tyr	Ile	Leu	Arg	Ala	Gln	Val	Ile		110	115		120
Asp	Ile	Ala	Thr	Gly	Arg	Ala	Val	Glu	Pro	Glu	Ser	Glu	Phe	Val		125	130		135
Ile	Lys	Val	Ser	Asp	Ile	Asn	Asp	Asn	Glu	Pro	Lys	Phe	Leu	Asp		140	145		150
Glu	Pro	Tyr	Glu	Ala	Ile	Val	Pro	Glu	Met	Ser	Pro	Glu	Gly	Thr		155	160		165
Leu	Val	Ile	Gln	Val	Thr	Ala	Ser	Asp	Ala	Asp	Asp	Pro	Ser	Ser		170	175		180
Gly	Asn	Asn	Ala	Arg	Leu	Leu	Tyr	Ser	Leu	Leu	Gln	Gly	Gln	Pro		185	190		195
Tyr	Phe	Ser	Val	Glu	Pro	Thr	Thr	Gly	Val	Ile	Arg	Ile	Ser	Ser		200	205		210
Lys	Met	Asp	Arg	Glu	Leu	Gln	Asp	Glu	Tyr	Trp	Val	Ile	Ile	Gln		215	220		225
Ala	Lys	Asp	Met	Ile	Gly	Gln	Pro	Gly	Ala	Leu	Ser	Gly	Thr	Thr		230	235		240
Ser	Val	Leu	Ile	Lys	Leu	Ser	Asp	Val	Asn	Asp	Asn	Lys	Pro	Ile		245	250		255
Phe	Lys	Glu	Ser	Leu	Tyr	Arg	Leu	Thr	Val	Ser	Glu	Ser	Ala	Pro		260	265		270
Thr	Gly	Thr	Ser	Ile	Gly	Thr	Ile	Met	Ala	Tyr	Asp	Asn	Asp	Ile		275	280		285

Gly	Glu	Asn	Ala	Glu	Met	Asp	Tyr	Ser	Ile	Glu	Glu	Asp	Asp	Ser		290	295	300
Gln	Thr	Phe	Asp	Ile	Ile	Thr	Asn	His	Glu	Thr	Gln	Glu	Gly	Ile		305	310	315
Val	Ile	Leu	Lys	Lys	Lys	Val	Asp	Phe	Glu	His	Gln	Asn	His	Tyr		320	325	330
Gly	Ile	Arg	Ala	Lys	Val	Lys	Asn	His	His	Val	Pro	Glu	Gln	Leu		335	340	345
Met	Lys	Tyr	His	Thr	Glu	Ala	Ser	Thr	Thr	Phe	Ile	Lys	Ile	Gln		350	355	360
Val	Glu	Asp	Val	Asp	Glu	Pro	Pro	Leu	Phe	Leu	Leu	Pro	Tyr	Tyr		365	370	375
Val	Phe	Glu	Val	Phe	Glu	Glu	Thr	Pro	Gln	Gly	Ser	Phe	Val	Gly		380	385	390
Val	Val	Ser	Ala	Thr	Asp	Pro	Asp	Asn	Arg	Lys	Ser	Pro	Ile	Arg		395	400	405
Tyr	Ser	Ile	Thr	Arg	Ser	Lys	Val	Phe	Asn	Ile	Asn	Asp	Asn	Gly		410	415	420
Thr	Ile	Thr	Thr	Ser	Asn	Ser	Leu	Asp	Arg	Glu	Ile	Ser	Ala	Trp		425	430	435
Tyr	Asn	Leu	Ser	Ile	Thr	Ala	Thr	Glu	Lys	Tyr	Asn	Ile	Glu	Gln		440	445	450
Ile	Ser	Ser	Ile	Pro	Leu	Tyr	Val	Gln	Val	Leu	Asn	Ile	Asn	Asp		455	460	465
His	Ala	Pro	Glu	Phe	Ser	Gln	Tyr	Tyr	Glu	Thr	Tyr	Val	Cys	Glu		470	475	480
Asn	Ala	Gly	Ser	Gly	Gln	Val	Ile	Gln	Thr	Ile	Ser	Ala	Val	Asp		485	490	495
Arg	Asp	Glu	Ser	Ile	Glu	Glu	His	His	Phe	Tyr	Phe	Asn	Leu	Ser		500	505	510
Val	Glu	Asp	Thr	Asn	Asn	Ser	Ser	Phe	Thr	Ile	Ile	Asp	Asn	Gln		515	520	525
Asp	Asn	Thr	Ala	Val	Ile	Leu	Thr	Asn	Arg	Thr	Gly	Phe	Asn	Leu		530	535	540
Gln	Glu	Glu	Pro	Val	Phe	Tyr	Ile	Ser	Ile	Leu	Ile	Ala	Asp	Asn		545	550	555
Gly	Ile	Pro	Ser	Leu	Thr	Ser	Thr	Asn	Thr	Leu	Thr	Ile	His	Val		560	565	570

Cys	Asp	Cys	Gly	Asp	Ser	Gly	Ser	Thr	Gln	Thr	Cys	Gln	Tyr	Gln	575	580	585
Glu	Leu	Val	Leu	Ser	Met	Gly	Phe	Lys	Thr	Glu	Val	Ile	Ile	Ala	590	595	600
Ile	Leu	Ile	Cys	Ile	Met	Ile	Ile	Phe	Gly	Phe	Ile	Phe	Leu	Thr	605	610	615
Leu	Gly	Leu	Lys	Gln	Arg	Arg	Lys	Gln	Ile	Leu	Phe	Pro	Glu	Lys	620	625	630
Ser	Glu	Asp	Phe	Arg	Glu	Asn	Ile	Phe	Gln	Tyr	Asp	Asp	Glu	Gly	635	640	645
Gly	Gly	Glu	Glu	Asp	Thr	Glu	Ala	Phe	Asp	Ile	Ala	Glu	Leu	Arg	650	655	660
Ser	Ser	Thr	Ile	Met	Arg	Glu	Arg	Lys	Thr	Arg	Lys	Thr	Thr	Ser	665	670	675
Ala	Glu	Ile	Arg	Ser	Leu	Tyr	Arg	Gln	Ser	Leu	Gln	Val	Gly	Pro	680	685	690
Asp	Ser	Ala	Ile	Phe	Arg	Lys	Phe	Ile	Leu	Glu	Lys	Leu	Glu	Glu	695	700	705
Ala	Asn	Thr	Asp	Pro	Cys	Ala	Pro	Pro	Phe	Asp	Ser	Leu	Gln	Thr	710	715	720
Tyr	Ala	Phe	Glu	Gly	Thr	Gly	Ser	Leu	Ala	Gly	Ser	Leu	Ser	Ser	725	730	735
Leu	Glu	Ser	Ala	Val	Ser	Asp	Gln	Asp	Glu	Ser	Tyr	Asp	Tyr	Leu	740	745	750
Asn	Glu	Leu	Gly	Pro	Arg	Phe	Lys	Arg	Leu	Ala	Cys	Met	Phe	Gly	755	760	765
Ser	Ala	Val	Gln	Ser	Asn	Asn									770		

<210> 265

<211> 349

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 24, 60, 141, 226, 228, 249, 252

<223> unknown base

<400> 265

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attcaagcca aggacatgat tggtcagcca ggagcgttgt ntggaacaac 150
aagtgtatta attaaacttt cagatgtaa tgacaataag cctatatatta 200
aagaaagttt ataccgcttg actgtntntg aatctgcacc cactgggant 250
tntataggaa caatcatggc atatgataat gacataggag agaatgcaga 300
aatggattac agcattgaag aggatgattc gcaaacattt gacattatt 349

<210> 266

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 266

cttgactgtc tctgaatctg ccccc 25

<210> 267

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 267

aagtgggtga agcctccagt gtgg 24

<210> 268

<211> 52

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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gc 52

<210> 269

<211> 2747

<212> DNA

<213> Homo sapiens

<400> 269

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acattgagat actatcatta acattaggac cttagaattt tgggtattgt 950
aatctgaagt atggtattac aaaacaaaca aacaaacaaa aaacccatgt 1000
gttaaaatac tcagtgttaa acatggctta atcttatttt atcttcttc 1050
ctcaatatag gaggaagat ttttccattt gtattactgc ttccattga 1100
gtaatcatalc tcaaatgggg gaaggggtgc tccttaaata tatatagata 1150
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cattatgttg atactagcat acttaaaata tctctaaaat aggtaaatgt 1250
atttaattcc atattgatga agatgtttat tggatatatt tctttttcgt 1300
ccttatatac atatgtaaca gtcaaatatc atttactctt cttcattagc 1350
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tttcaattct tcatgcgtgc cttttcata tacttatttt attttttacc 1450
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gtttctaaag ccaagaagaa ttattacaa atcagaactt tggaggcaaa 1600

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<210> 270

<211> 211

<212> PRT

<213> Homo sapiens

<400> 270

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Leu Gly Trp Ile Gly Ala Ile Val Ser Thr Ala Leu Pro Gln Trp

20										25					30				
Arg	Ile	Tyr	Ser	Tyr	Ala	Gly	Asp	Asn	Ile	Val	Thr	Ala	Gln	Ala					
				35					40					45					
Met	Tyr	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Ser	Gln	Ser	Thr	Gly					
				50					55					60					
Gln	Ile	Gln	Cys	Lys	Val	Phe	Asp	Ser	Leu	Leu	Asn	Leu	Ser	Ser					
				65					70					75					
Thr	Leu	Gln	Ala	Thr	Arg	Ala	Leu	Met	Val	Val	Gly	Ile	Leu	Leu					
				80					85					90					
Gly	Val	Ile	Ala	Ile	Phe	Val	Ala	Thr	Val	Gly	Met	Lys	Cys	Met					
				95					100					105					
Lys	Cys	Leu	Glu	Asp	Asp	Glu	Val	Gln	Lys	Met	Arg	Met	Ala	Val					
				110					115					120					
Ile	Gly	Gly	Ala	Ile	Phe	Leu	Leu	Ala	Gly	Leu	Ala	Ile	Leu	Val					
				125					130					135					
Ala	Thr	Ala	Trp	Tyr	Gly	Asn	Arg	Ile	Val	Gln	Glu	Phe	Tyr	Asp					
				140					145					150					
Pro	Met	Thr	Pro	Val	Asn	Ala	Arg	Tyr	Glu	Phe	Gly	Gln	Ala	Leu					
				155					160					165					
Phe	Thr	Gly	Trp	Ala	Ala	Ala	Ser	Leu	Cys	Leu	Leu	Gly	Gly	Ala					
				170					175					180					
Leu	Leu	Cys	Cys	Ser	Cys	Pro	Arg	Lys	Thr	Thr	Ser	Tyr	Pro	Thr					
				185					190					195					
Pro	Arg	Pro	Tyr	Pro	Lys	Pro	Ala	Pro	Ser	Ser	Gly	Lys	Asp	Tyr					
				200					205					210					

Val

<210> 271

<211> 564

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 21, 69, 163, 434, 436, 444

<223> unknown base

<400> 271

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ggatggatcg gcgccatcnt cacactgccc ttccccagtg gaggatttta 100

ctccctatgc tggcgacaac atcgtgaccg cccagcccat gtacgagggg 150

ctgtggatgt ccngcgtgtc gcagagcacc gggcagatcc agtgcaaagt 200
 ctttgactcc ttgctgaatc tgagcagcac attgcaagca acccgtgcct 250
 tgatgggtgtg tggcatcctc ctgggagtga tagcaatctt tgtggccacc 300
 gttggcatga agtgtatgaa gtgcttgaa gacgatgagg tgcagaagat 350
 gaggatggct gtcattgggg gcgcgatatt tcttcttgca ggtctggcta 400
 ttttagttgc cacagcatgg tatggcaata gaancnttca acanttctat 450
 gaccctatga cccagtc aa tgccaggtac gaatttggtc aggtctctct 500
 cactggctgg gctgctgctt ctctctgcct tctgggaggt gccctacttt 550
 gctgttctctg tccc 564

<210> 272

<211> 498

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 49, 102, 141, 147, 171, 324-325, 339-341

<223> unknown base

<400> 272

acccttgacc caacgcggcc ccccgaccgn ttcattggcca aacgcgggnc 50
 tccagctgtt gggcttcatt ctccccttcc tgggatggac cggcgcccat 100
 cntcagcaact gccctgcccc agtggaggat ttactcctat nccggcnaca 150
 acatcgtgac cgcccaggcc ntgtacgagg ggctgtggat gtcttgctg 200
 tcgcagagca ccgggcagat ccagtgcaaa gtctttgact cccttgctga 250
 atctgagcag cacattgcaa gcaaccctg ccttgatggt ggttggcatc 300
 ctctggggag tgatagcaat cttnttggcc accgttgtnn ntgaagtgt 350
 tgaagtgcct ggaagacgat gaggtgcaga agatgaggat ggctgtcatt 400
 gggggcgcca tatttcttct tgcaggtctg gctatttttag ttgccacagc 450
 atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccga 498

<210> 273

<211> 552

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394

<223> unknown base

<400> 273

gggcccgacc attatccaac cgggntcact gttggctcat ctccctcctg 50
gatgaancgc gccatcntca gactccctgc cccatggaga tttnnccctat 100
gctggcgaca acatcntgac cccagccat gtacgagggg ctttgaacgt 150
cngcgtgtcg cagancaccg ggcagatcca gtgcaaagtc tttgactcct 200
tgctgaatct gngcagcaca ttgcagcaac cntgcccctg atggtgggtg 250
gcatectcct gggagtata gcaatctttg tggccaccgt tggcatgaag 300
tgtatgaagt gcttgaaga cgatgaggtg cagaagatga ggatggctgt 350
cattgggggc gcgatatttc ttcttgacag tctggctatt tnnngttgcc 400
acagcatggt atggcaatag aatcggtcaa gaattctatg accctatgac 450
cccagtcaat gccaggtacg aatttggta ggctctcttc actggctggg 500
ctgctgcttc tctctgcctt ctgggaggtg cctactttg ctgttcctgc 550
ga 552

<210> 274

<211> 526

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407

<223> unknown base

<400> 274

attctcccct cctggatgga tcgcnccacc gtcacattgc ctccccccan 50
tggaggattn actcctatgc tggcgacaac atcgtgaccc cccaggccat 100
ttaccgaggg gctttggatg tcntgcntgt cgagagcac cgggcagatc 150
ccagtcaaaa gtctttgact ccttgctgaa tctgagcagc acattgcaag 200
caaccgtgc cttgatgggg ttggcatcct cctgggagtg atagcaacct 250
ttgtggccac cgttggcatg aagtgtatga agtgcttga agacgatgag 300
gtgccagaag atgaggatgg ctgtcattgg gggcgcgata tttcttggtg 350
caggtctggc tattttagtn gccacagcat ggtatggcaa tagantnntt 400
cnnnnntct atgaccctat gacccagtc aatgccaggt acgaatttgg 450

tcaggtcttc ttcactggct gggtgctgc ttctctctgc cttctgggag 500
gtgccctact ttgctgttcc tgtccc 526

<210> 275
<211> 398
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274
<223> unknown base

<400> 275
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gcagcacatt ncaagcaacc cttgccttg aagggtggtg ncatcccccc 100
tgggagtga tagcaatctt tgtggccacc gttggcatga agtntatgaa 150
gtgcttgga gacgatgagg tgcagaagat gaggatggct gtcattgggg 200
gcgcgatatt tcttcttgca ggtctggcta ttttagtnnc cacagcatgg 250
tatggcaata gnatnnttcg nggnttctat gaccctatga cccagtcaa 300
tgccaggtag gaatttggtc aggtctctct cactggctgg gctgctgctt 350
ctctctgcct tctgggaggt gccctacttt gctgttctctg tccccgaa 398

<210> 276
<211> 495
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476
<223> unknown base

<400> 276
agcaatgccc tgccccagt ggaggattaa ttcctatgnt ggggacaaca 50
ttgtgacngc ccaggccatg tacggggggc tgtggatgtc ctgcgtgtcg 100
cagagcaccg ggcagatcca gtgcaaagtn tttgactcct tgctgaattt 150
gagcagcaca ttgcaagcaa cccgtgcctt gatgggtggtt ggcattcttc 200
tgggagtgat agcaatcttt gtggccaccg tggnaatgaa gtgtatgaag 250
tgcttggaag acgatgaggt gcagaagatg aggatggctg tcattggggg 300
cgcgatattt cttnttgcat gtctggctat tttagttgcc acagcatggt 350
atggcaatag aatngttcaa gaattttatg accctatgac cccagtcaat 400

gccaggtacg aatttgggtca ggctttnttc actggctggg ctgctgcttn 450

tttctgcctt ntgggaggtg ccctantttg ctgttcctgc gaacc 495

<210> 277

<211> 200

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 34, 87, 138, 147, 163, 165-166, 172

<223> unknown base

<400> 277

tcataggggg gcgcgatatt ttttcttgca ggtntgggta ttttagttgc 50

cacagcatgg tatggcaata gaatcgttca agaattntat gaccctatga 100

ccccagtcaa tgccaggtac gaatttggtc aggctctntt cactggntgg 150

gctgctgctt ctntnngcct tntgggaggt gccctacttt gctgttcctg 200

<210> 278

<211> 542

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 26, 43, 55, 77, 198, 361-362, 391-392, 396

<223> unknown base

<400> 278

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ttacnctat gctggcgaac aacatcntga ccgccaggc catgtacgag 100

gggctgtgga atgtcctgcg tgtcccagag caccgggcag atccagtgc 150

aagtctttga ctcttgctg aatctgagca gcacattgca agcaacctg 200

ccttgatggg ggttggcatc ctctgggag tgatagcaat ctttgtggcc 250

accgttggca tgaaagtgtg tgaagtgctt ggaagacgat gaggtgcaga 300

agatgaggat ggctgtcatt gggggcgcga tatttcttct tgcaggctctg 350

gctatttttag nngccacagc atggtatggc aatcagaccc nntcanaaac 400

tctatgaccc tatgacccca gtcaatgccca ggtacgaatt tggtcaggct 450

ctcttcaactg gctgggctgc tgcttctctc tgccttcttg gaggtgccct 500

actttgctgt tctgtcccc gaaaaacaac ctcttaccga cg 542

<210> 279
<211> 548
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 90, 115, 147, 228, 387
<223> unknown base

<400> 279
cggggctgca gctggtgggc ttcattctgc ttcctgggat ggaatcggcg 50
ccatcgctcag cactgccctg ccccatggag gatttactcn tatgctggcg 100
acaacatcgt gaccncccag gccatgtacg aggggctgtg gatgtcngcg 150
tgtcgcagag caccgggcag atccagtgc aagtctttga ctcttgctg 200
aatctgagca gcacattgca agcaacctg ccttgatggt ggttggcatc 250
ctcctgggag tgatagcaat ctttgtggcc accgttggca tgaagtgtat 300
gaagtgcttg gaagacgatg aggtgcagaa gatgaggatg gctgtcattg 350
ggggcgcgat atttcttctt gcaggtcttg ctatttntag ttgccacagc 400
atggtatggc aatagaatcg ttcaagaatt ctatgacct atgaccccag 450
tcaatgccag gtacgaatct ggtcaggctc tcttcaactg ctgggctgct 500
gcttctctct gccttctggg aggtgcccta ctttgcgtgt cctgcgaa 548

<210> 280
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 280
cgagcgagtc atggccaacg c 21

<210> 281
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 281
gtgtcacacg tagtctttcc cgctgg 26

<210> 282
<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 282

ctgcagctgt tgggcttcat tctgccttc ctgggatgga tcg 43

<210> 283

<211> 2285

<212> DNA

<213> Homo sapiens

<400> 283

gcgtgccgtc agctcgccgg gcaccgcggc ctgccctcg ccctccgccc 50
ctgcgcctgc accgcgtaga ccgaccccc cctccagcgc gccacccgg 100
tagaggaccc ccgcccgtgc ccgaccgggt cccgccttt ttgtaaaact 150
taaagcgggc gcagcattaa cgcttccgc cccggtgacc tctcaggggt 200
ctccccgcca aagggtgctc gccgctaagg aacatggcga aggtggagca 250
ggtcctgagc ctcgagccgc agcacgagct caaattccga ggtcccttca 300
ccgatgttgt caccaccaac ctaaagcttg gcaaccogac agaccgaaat 350
gtgtgtttta aggtgaagac tacagcacca cgtaggtact gtgtgaggcc 400
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tacagccttt cgattatgat cccaatgaga aaagtaaaca caagtttatg 500
gttcagtcta tgtttgctcc aactgacact tcagatatgg aagcagtatg 550
gaaggaggca aaaccggaag accttatgga ttcaaaactt agatgtgtgt 600
ttgaattgcc agcagagaat gataaaccac atgatgtaga aataaataaa 650
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tctgagttct tctttggatg acaccgaagt taagaagggt atggaagaat 750
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ggctcttggc tctggtggtt ttgttcttta tcgttggtgt aattattggg 950
aagattgcct tgtagaggta gcatgcacag gatggtaaata tggattggtg 1000
gatccaccat atcatgggat ttaaatttat cataaccatg tgtaaaaaga 1050

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agaaaaatta taataaagcc ccaaaattaa gaaaa 2285

<210> 284

<211> 243

<212> PRT

<213> Homo sapiens

<400> 284

Met Ala Lys Val Glu Gln Val Leu Ser Leu Glu Pro Gln His Glu

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Leu Lys Phe Arg Gly Pro Phe Thr Asp Val Val Thr Thr Asn Leu	20	25	30
Lys Leu Gly Asn Pro Thr Asp Arg Asn Val Cys Phe Lys Val Lys	35	40	45
Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly Ile	50	55	60
Ile Asp Ala Gly Ala Ser Ile Asn Val Ser Val Met Leu Gln Pro	65	70	75
Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val	80	85	90
Gln Ser Met Phe Ala Pro Thr Asp Thr Ser Asp Met Glu Ala Val	95	100	105
Trp Lys Glu Ala Lys Pro Glu Asp Leu Met Asp Ser Lys Leu Arg	110	115	120
Cys Val Phe Glu Leu Pro Ala Glu Asn Asp Lys Pro His Asp Val	125	130	135
Glu Ile Asn Lys Ile Ile Ser Thr Thr Ala Ser Lys Thr Glu Thr	140	145	150
Pro Ile Val Ser Lys Ser Leu Ser Ser Ser Leu Asp Asp Thr Glu	155	160	165
Val Lys Lys Val Met Glu Glu Cys Lys Arg Leu Gln Gly Glu Val	170	175	180
Gln Arg Leu Arg Glu Glu Asn Lys Gln Phe Lys Glu Glu Asp Gly	185	190	195
Leu Arg Met Arg Lys Thr Val Gln Ser Asn Ser Pro Ile Ser Ala	200	205	210
Leu Ala Pro Thr Gly Lys Glu Glu Gly Leu Ser Thr Arg Leu Leu	215	220	225
Ala Leu Val Val Leu Phe Phe Ile Val Gly Val Ile Ile Gly Lys	230	235	240

Ile Ala Leu

<210> 285

<211> 418

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 40, 53, 68, 119, 134, 177-178, 255

<223> unknown base

<400> 285

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ctggagtcag gacaatggnt cgggctgcag aggnntagaa gcgagggcac 150
cagcagtttt ggggtggggag caagggngga gagaaactct tcagcgaatc 200
cttctagtag tagttgagag ttgactgtg aattaatttt atgccataaa 250
agacnaaccc agttctgttt gactatgtag catcttgaaa agaaaaatta 300
taataaagcc ccaaaattaa gaattctttt gtcattttgt cacatttgct 350
ctatgggggg aattattatt ttatcatttt tattattttg ccattggaag 400
gttaacttta aaatgagc 418

<210> 286

<211> 543

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 73, 97

<223> unknown base

<400> 286

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gggagctgga gccccagcat gctggggagt gcggtcagct ccacacagta 150
gtccccacgt ggcccactcc cggcccaggc tgctttccgt gtcttcagtt 200
ctgtccaagc catcagctcc ttgggactga tgaacagagt cagaagccca 250
aaggaattgc cactgtggca gcatcagacg tactcgtcat aagtgagagg 300
cgtgtgttga ctgattgacc cagcgctttg gaaataaatg gcagtgcttt 350
gttcacttaa agggaccaag cttaaattgta ttggttcatg tagtgaagtc 400
aaactgttat tcagagatgt ttaatgcata tttaacttat ttaatgtatt 450
tcatctcatg ttttcttatt gtcacaagag tacagttaat gctgcgtgct 500
gctgaactct gttgggtgaa ctggtattgc tgctggaggg ctg 543

<210> 287

<211> 270

<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242
<223> unknown base

<400> 287
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ctttagtagagg tagnatgcac cnggctggta aattggattg gtggatccac 100
catatccatg ggattttaaatt ttatcataac catgtgtaaa aagaaattaa 150
tgtatgatga catntcacag gtattgcctt taaattaccc atccctgnan 200
acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250
agttaaaaaat gtatagtaac 270

<210> 288
<211> 428
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 35, 116, 129, 197, 278, 294, 297, 349, 351
<223> unknown base

<400> 288
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gccatcagct ccttgggact gatgaacaga gtcagaagcc caaaggaatt 100
gcactgtggc agcatnagac gtacttgtna taagtgagag gcgtgtgttg 150
actgattgac ccagcgcttt ggaaataaat ggcagtgcct tgttcantta 200
aagggaccaa gctaaatttg tattggttca tgtagtgaag tcaaactgtt 250
attcagagat gtttaatgca tatttaantt atttaatgta tttnatntca 300
tgttttctta ttgtcacaag agtacagtta atgctgcgtg ctgctgaant 350
ntgttggttg aactggtatt gctgctggag ggctgtgggc tcctctgtct 400
ttggagagtc tggatcatgtg gaggtggg 428

<210> 289
<211> 320
<212> DNA
<213> Homo sapiens

<400> 289
tgctttccgt gtcttcagtt ctgtccaagc catcagctcc ttgggacttg 50

atgaacagag tcagaagccc aaaggaattg cactgtggca gcatcagacg 100
tactcgtcat aagtgagagg cgtgtgttga ctgattgacc cagcgctttg 150
gaaataaatg gcagtgcctt gtccacttaa agggaccaag ctaaatttgt 200
attggttcat gtagtgaagt caaactgtta ttcagagatg tttaatgcat 250
atttaactta tttaatgtat ttcattctcat gttttcttat tgtcacaaga 300
gtacagttaa tgctgcgtgc 320

<210> 290

<211> 609

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,
447, 481, 513, 532, 584, 598

<223> unknown base

<400> 290

aaacctttaa aagttgaggg gaaaagaatg atcctttatt aatgacaagg 50
gaaacntgn gtaatgccac aatggcatat tgtaaattgc attttaaaaca 100
ttggtaggcc ttggtacatg atgctggatt acctctctta aaatgacacc 150
cttcctcgcc tgttggtgct ggcccttggg gagctngagc ccagcatgct 200
ggggagtgcg gtctgctcca cacagtagtc ccangtggc ccantcccgg 250
cccaggctgc tttccgtgtc ttcagttctg tccaagccat cagctccttg 300
ggantgatga acagagtcag aagcccaaag gaattgcant gtggcagcat 350
cagangtant ngtcataagt gagaggcgtg tgttgantga ttgaccagc 400
gctttggaaa taaatggcag tgctttgttc anttaaaggg nccaagntaa 450
atttgtattg gttcatgtag tgaagtcaaa ntgttattca gagatgttta 500
atgcatattt aanttattta atgtatttca tntcatgttt tottattgtc 550
acaagggtag agttaatgct gcgtgctgct gaantctgtt gggtagaantg 600
gtattgctg 609

<210> 291

<211> 493

<212> DNA

<213> Homo sapiens

<400> 291

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cacagtagtc cccacgtggc ccaactcccgg cccaggetgc tttccgtgtc 100
ttcagttctg tccaagccat cagctccttg ggactgatga acagagtcag 150
aagcccaaag gaattgcact gtggcagcat cagacgtact cgtcataagt 200
gagagggcgtg tgttgactga ttgaccagc gctttggaaa taaatggcag 250
tgctttgttc acttaaagg accaagctaa atttgtattg gttcatgtag 300
tgaagtcaaa ctgttattca gagatgttta atgcatattt aacttattta 350
atgtatttca tctcatgttt tcttattgtc acaagagtac agttaatgct 400
gcgtgctgct gaactctgtt gggatgaactg gtattgctgc tggagggctg 450
tgggctcctc tgtctctgga gagtctggc atgtggaggt ggg 493

<210> 292

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 292

gcaccaccgt aggtacttgt gtgaggc 27

<210> 293

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

aaccaccaga gccaagagcc ggg 23

<210> 294

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cagcggaatc atcgatgcag gggcctcaat taatgtatct gtgatgttac 50

<210> 295

<211> 2530

<212> DNA

<213> Homo sapiens

<400> 295

gcgagctccg ggtgctgtgg cccggccttg gcggggcggc ctccggctca 50
ggctggctga gaggtccca gctgcagcgt ccccgccgc ctctcgga 100
gctctgatct cagctgacag tgccctcggg gaccaaaca gcctggcagg 150
gtctcacttt gttgcccagg ctggagttca gtgccatgat catggtttac 200
tgcagccttg acctcctggg ttcaagcgat cctgctgagt agctgggact 250
acaggacaaa attagaagat caaaatggaa aatatgctgc tttggttgat 300
atthttcacc cctgggtgga ccctcattga tggatctgaa atggaatggg 350
atthttatgtg gcacttgaga aaggtacccc ggattgtcag tgaaaggact 400
ttccatctca ccagcccccgc atttgaggca gatgctaaga tgatggtaaa 450
tacagtgtgt ggcattcgaat gccagaaaga actcccaact cccagccttt 500
ctgaattgga ggattatctt tcctatgaga ctgtctttga gaatggcacc 550
cgaaccttaa ccagggtgaa agttcaagat ttggttcttg agccgactca 600
aaatatcacc acaaaggag tatctgttag gagaaagaga caggtgtatg 650
gcaccgacag caggttcagc atcttgga aaaggttctt aaccaatttc 700
cctttcagca cagctgtgaa gctttccacg ggctgtagtg gcattctcat 750
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tggatgtcca cgggggttcag aaggactaca acgttgctgt tcgcatcact 1450
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 aatgtgaaat tgcatagata aaggtagatg gtaaagcaat tagtatcaga 1950
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 ttcagctcat gccctcaatg tttatattgt gttatctggt gggctctggga 2050
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 cttcaciaaat tatgaatgat catgtgttga aagccacatt attttatgct 2350
 atacattcta tgtatgaggt gctacatttt taggacaaaag aattctgtaa 2400
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 cctaaaaatg aataaaattt atgaatatga 2530

<210> 296

<211> 413

<212> PRT

<213> Homo sapiens

<400> 296

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Thr Leu Ile Asp Gly Ser Glu Met Glu Trp Asp Phe Met Trp His

20	25	30
Leu Arg Lys Val Pro Arg Ile Val Ser Glu Arg Thr Phe His Leu		
35	40	45
Thr Ser Pro Ala Phe Glu Ala Asp Ala Lys Met Met Val Asn Thr		
50	55	60
Val Cys Gly Ile Glu Cys Gln Lys Glu Leu Pro Thr Pro Ser Leu		
65	70	75
Ser Glu Leu Glu Asp Tyr Leu Ser Tyr Glu Thr Val Phe Glu Asn		
80	85	90
Gly Thr Arg Thr Leu Thr Arg Val Lys Val Gln Asp Leu Val Leu		
95	100	105
Glu Pro Thr Gln Asn Ile Thr Thr Lys Gly Val Ser Val Arg Arg		
110	115	120
Lys Arg Gln Val Tyr Gly Thr Asp Ser Arg Phe Ser Ile Leu Asp		
125	130	135
Lys Arg Phe Leu Thr Asn Phe Pro Phe Ser Thr Ala Val Lys Leu		
140	145	150
Ser Thr Gly Cys Ser Gly Ile Leu Ile Ser Pro Gln His Val Leu		
155	160	165
Thr Ala Ala His Cys Val His Asp Gly Lys Asp Tyr Val Lys Gly		
170	175	180
Ser Lys Lys Leu Arg Val Gly Leu Leu Lys Met Arg Asn Lys Ser		
185	190	195
Gly Gly Lys Lys Arg Arg Gly Ser Lys Arg Ser Arg Arg Glu Ala		
200	205	210
Ser Gly Gly Asp Gln Arg Glu Gly Thr Arg Glu His Leu Gln Glu		
215	220	225
Arg Ala Lys Gly Gly Arg Arg Arg Lys Lys Ser Gly Arg Gly Gln		
230	235	240
Arg Ile Ala Glu Gly Arg Pro Ser Phe Gln Trp Thr Arg Val Lys		
245	250	255
Asn Thr His Ile Pro Lys Gly Trp Ala Arg Gly Gly Met Gly Asp		
260	265	270
Ala Thr Leu Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Arg Ala		
275	280	285
His Lys Lys Lys Tyr Met Glu Leu Gly Ile Ser Pro Thr Ile Lys		
290	295	300
Lys Met Pro Gly Gly Met Ile His Phe Ser Gly Phe Asp Asn Asp		

305										310					315				
Arg	Ala	Asp	Gln	Leu	Val	Tyr	Arg	Phe	Cys	Ser	Val	Ser	Asp	Glu					
				320					325					330					
Ser	Asn	Asp	Leu	Leu	Tyr	Gln	Tyr	Cys	Asp	Ala	Glu	Ser	Gly	Ser					
			335					340						345					
Thr	Gly	Ser	Gly	Val	Tyr	Leu	Arg	Leu	Lys	Asp	Pro	Asp	Lys	Lys					
			350					355						360					
Asn	Trp	Lys	Arg	Lys	Ile	Ile	Ala	Val	Tyr	Ser	Gly	His	Gln	Trp					
			365					370						375					
Val	Asp	Val	His	Gly	Val	Gln	Lys	Asp	Tyr	Asn	Val	Ala	Val	Arg					
			380					385						390					
Ile	Thr	Pro	Leu	Lys	Tyr	Ala	Gln	Ile	Cys	Leu	Trp	Ile	His	Gly					
			395					400						405					
Asn	Asp	Ala	Asn	Cys	Ala	Tyr	Gly												
			410																

<210> 297

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 297

gcatctgcag gagagagcga aggg 24

<210> 298

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 298

catcgttccc gtgaatccag aggc 24

<210> 299

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 299

gaagggaggc cttcctttca gtggaccgg gtcaagaata cccac 45

<210> 300

<211> 1869
<212> DNA
<213> Homo sapiens

<400> 300

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ccagtactgg atgtgacagc aggcagagga gcacttagca gcttattcag 100
tgtccgattc tgattccggc aaggatccaa gcatggaatg ctgccgtcgg 150
gcaactcctg gcacactgct cctctttctg gctttcctgc tcctgagttc 200
caggaccgca cgctccgagg aggaccggga cggcctatgg gatgcctggg 250
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cagaacatgc agtaatgtgg actgccacc agaagcaggt gatttccgag 400
ctcagcaatg ctcagctcat aatgatgtca agcaccatgg ccagttttat 450
gaatggcttc ctgtgtctaa tgaccctgac aacctatgtt cactcaagtg 500
ccaagccaaa ggaacaacc tggttgttga actagcacct aaggtcttag 550
atggtaacgg ttgtatata gaatctttgg atatgtgcat cagtggttta 600
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cagaaatttc cagacaaaga gatactgaga atggctggac cactcacagc 950
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gatccttgct cagccagtga cggatacaag cagatcatgc cttatgacct 1250
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cctcgtgtgg ggggggcatc cagagccggg cagtttctctg tgtggaggag 1350
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 ccctaagatg cccatcgcgc agccctgcaa cttttttgac tgccctaaat 1450
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 agataccgtg tggctcctctg catcgacatc cgaggaatgc acacaggagg 1550
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 gtttaaagaa agcagtgtct cactggttgt agctttcatg ggttctgaac 1800
 taagtgtaat catctcacca aagctttttg gctctcaaat taaagattga 1850
 ttagtttcaa aaaaaaaaaa 1869

<210> 301
 <211> 525
 <212> PRT
 <213> Homo sapiens

<400> 301
 Met Glu Cys Cys Arg Arg Ala Thr Pro Gly Thr Leu Leu Leu Phe
 1 5 10 15
 Leu Ala Phe Leu Leu Leu Ser Ser Arg Thr Ala Arg Ser Glu Glu
 20 25 30
 Asp Arg Asp Gly Leu Trp Asp Ala Trp Gly Pro Trp Ser Glu Cys
 35 40 45
 Ser Arg Thr Cys Gly Gly Gly Ala Ser Tyr Ser Leu Arg Arg Cys
 50 55 60
 Leu Ser Ser Lys Ser Cys Glu Gly Arg Asn Ile Arg Tyr Arg Thr
 65 70 75
 Cys Ser Asn Val Asp Cys Pro Pro Glu Ala Gly Asp Phe Arg Ala
 80 85 90
 Gln Gln Cys Ser Ala His Asn Asp Val Lys His His Gly Gln Phe
 95 100 105
 Tyr Glu Trp Leu Pro Val Ser Asn Asp Pro Asp Asn Pro Cys Ser
 110 115 120
 Leu Lys Cys Gln Ala Lys Gly Thr Thr Leu Val Val Glu Leu Ala
 125 130 135

Pro Lys Val Leu Asp Gly Thr Arg Cys Tyr Thr Glu Ser Leu Asp	140	145	150
Met Cys Ile Ser Gly Leu Cys Gln Ile Val Gly Cys Asp His Gln	155	160	165
Leu Gly Ser Thr Val Lys Glu Asp Asn Cys Gly Val Cys Asn Gly	170	175	180
Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr Lys Ser Gln	185	190	195
Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala Leu Pro Tyr	200	205	210
Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp His Leu	215	220	225
Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser	230	235	240
Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp	245	250	255
Phe Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro	260	265	270
Leu Thr Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala	275	280	285
Asp Ser Thr Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg	290	295	300
Trp Arg Glu Thr Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly	305	310	315
Gly Tyr Gln Leu Thr Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn	320	325	330
Arg Val Val Ala Asp Gln Tyr Cys His Tyr Tyr Pro Glu Asn Ile	335	340	345
Lys Pro Lys Pro Lys Leu Gln Glu Cys Asn Leu Asp Pro Cys Pro	350	355	360
Ala Ser Asp Gly Tyr Lys Gln Ile Met Pro Tyr Asp Leu Tyr His	365	370	375
Pro Leu Pro Arg Trp Glu Ala Thr Pro Trp Thr Ala Cys Ser Ser	380	385	390
Ser Cys Gly Gly Gly Ile Gln Ser Arg Ala Val Ser Cys Val Glu	395	400	405
Glu Asp Ile Gln Gly His Val Thr Ser Val Glu Glu Trp Lys Cys	410	415	420

Met	Tyr	Thr	Pro	Lys	Met	Pro	Ile	Ala	Gln	Pro	Cys	Asn	Ile	Phe	425	430	435
Asp	Cys	Pro	Lys	Trp	Leu	Ala	Gln	Glu	Trp	Ser	Pro	Cys	Thr	Val	440	445	450
Thr	Cys	Gly	Gln	Gly	Leu	Arg	Tyr	Arg	Val	Val	Leu	Cys	Ile	Asp	455	460	465
His	Arg	Gly	Met	His	Thr	Gly	Gly	Cys	Ser	Pro	Lys	Thr	Lys	Pro	470	475	480
His	Ile	Lys	Glu	Glu	Cys	Ile	Val	Pro	Thr	Pro	Cys	Tyr	Lys	Pro	485	490	495
Lys	Glu	Lys	Leu	Pro	Val	Glu	Ala	Lys	Leu	Pro	Trp	Phe	Lys	Gln	500	505	510
Ala	Gln	Glu	Leu	Glu	Glu	Gly	Ala	Ala	Val	Ser	Glu	Glu	Pro	Ser	515	520	525

<210> 302
 <211> 1533
 <212> DNA
 <213> Homo sapiens

<400> 302
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 ctgggcgggg cgtgtgtggt ggcggcccg cggttcgtgg ggcccagggt 150
 ccagcggctg cgcagaggcg gggaccccg cctcatgcac gggaagactg 200
 tgctgatcac cggggcgaac agcggcctgg gccgcgccac ggccgccgag 250
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 tccagtcccc ttacatgaag actgaagatg ggtttgagat gcagttcgga 550
 gtgaaccatc tggggcactt tctactcacc aatcttctcc ttggactcct 600
 caaaagttca gctcccagca ggattgtggt agtttcttcc aaactttata 650
 aatacggaga catcaatctt gatgacttga acagtgaaca aagctataat 700
 aaaagctttt gttatagccg gagcaaactg gctaacattc tttttaccag 750

ggaactagcc cgccgcttag aaggcacaaa tgtcacogtc aatgtgttgc 800
 atcctgggtat tgtacggaca aatctgggga ggcacataca cattccactg 850
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 agtagaaggt gccagactt ccattttattt ggctctttca cctgaggtag 950
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 taaaactgca tatcagttat atctgtgatc aggaatggtg tggattgaga 1150
 acttgttact tgaagaaaaa gaattttgat attggaatag cctgctaaga 1200
 ggtacatgtg ggtattttgg agttactgaa aaattatttt tgggataaga 1250
 gaatttcagc aaagatgttt taaatatata tagtaagtat aatgaataat 1300
 aagtacaatg aaaaatacaa ttatattgta aaattataac tgggcaagca 1350
 tggatgacat attaatatat gtcagaatta agtgactcaa agtgctatcg 1400
 agagggtttt caagtatctt tgagtttcat ggccaaagtg ttaactagtt 1450
 ttactacaat gtttgggtgtt tgtgtggaaa ttatctgcct ggtgtgtgca 1500
 cacaagtctt acttgaata aatttactgg tac 1533

<210> 303

<211> 336

<212> PRT

<213> Homo sapiens

<400> 303

Met	Ala	Val	Ala	Thr	Ala	Ala	Ala	Val	Leu	Ala	Ala	Leu	Gly	Gly	1	5	10	15
Ala	Leu	Trp	Leu	Ala	Ala	Arg	Arg	Phe	Val	Gly	Pro	Arg	Val	Gln	20	25	30	
Arg	Leu	Arg	Arg	Gly	Gly	Asp	Pro	Gly	Leu	Met	His	Gly	Lys	Thr	35	40	45	
Val	Leu	Ile	Thr	Gly	Ala	Asn	Ser	Gly	Leu	Gly	Arg	Ala	Thr	Ala	50	55	60	
Ala	Glu	Leu	Leu	Arg	Leu	Gly	Ala	Arg	Val	Ile	Met	Gly	Cys	Arg	65	70	75	
Asp	Arg	Ala	Arg	Ala	Glu	Glu	Ala	Ala	Gly	Gln	Leu	Arg	Arg	Glu	80	85	90	
Leu	Arg	Gln	Ala	Ala	Glu	Cys	Gly	Pro	Glu	Pro	Gly	Val	Ser	Gly				

	95	100	105
Val Gly Glu Leu Ile Val Arg Glu Leu Asp Leu Ala Ser Leu Arg	110	115	120
Ser Val Arg Ala Phe Cys Gln Glu Met Leu Gln Glu Glu Pro Arg	125	130	135
Leu Asp Val Leu Ile Asn Asn Ala Gly Ile Phe Gln Cys Pro Tyr	140	145	150
Met Lys Thr Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His	155	160	165
Leu Gly His Phe Leu Leu Thr Asn Leu Leu Leu Gly Leu Leu Lys	170	175	180
Ser Ser Ala Pro Ser Arg Ile Val Val Val Ser Ser Lys Leu Tyr	185	190	195
Lys Tyr Gly Asp Ile Asn Phe Asp Asp Leu Asn Ser Glu Gln Ser	200	205	210
Tyr Asn Lys Ser Phe Cys Tyr Ser Arg Ser Lys Leu Ala Asn Ile	215	220	225
Leu Phe Thr Arg Glu Leu Ala Arg Arg Leu Glu Gly Thr Asn Val	230	235	240
Thr Val Asn Val Leu His Pro Gly Ile Val Arg Thr Asn Leu Gly	245	250	255
Arg His Ile His Ile Pro Leu Leu Val Lys Pro Leu Phe Asn Leu	260	265	270
Val Ser Trp Ala Phe Phe Lys Thr Pro Val Glu Gly Ala Gln Thr	275	280	285
Ser Ile Tyr Leu Ala Ser Ser Pro Glu Val Glu Gly Val Ser Gly	290	295	300
Arg Tyr Phe Gly Asp Cys Lys Glu Glu Glu Leu Leu Pro Lys Ala	305	310	315
Met Asp Glu Ser Val Ala Arg Lys Leu Trp Asp Ile Ser Glu Val	320	325	330
Met Val Gly Leu Leu Lys	335		

<210> 304

<211> 521

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 20, 34, 62, 87, 221, 229

<223> unknown base

<400> 304

ggggattgta aagaggaagn actgtgccca aagntatgga tgaatctgtt 50
gcaagaaaat tntgggatat cagtgaagtg atggttngcc tgctaaaata 100
ggaacaagga gtaaaagagc tgtttataaa actgcatatc agttatatct 150
gtgatcagga atggtgtgga ttgagaactt gttacttgaa gaaaaagaat 200
tttgatattg gaatagcctg ntaagaggna catgtgggta ttttggagtt 250
actgaaaaat tatTTTTTggg ataagagaat ttcagcaaag atgttttaaa 300
tatatatagt aagtataatg aataataagt acaatgaaaa atacaattat 350
attgtaaaat tataactggg caagcatgga tgacatatta atatttgtca 400
gaattaagtg actcaaagtg ctatcgagag gtttttcaag tatctttgag 450
tttcatggcc aaagtgttaa ctagttttac tacaatgttt ggtgtttgtg 500
tggaaattat ctgcctggct t 521

<210> 305

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 305

ccaggaaatg ctccaggaag agcc 24

<210> 306

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 306

gcccattgaca ccaaattgaa gagtgg 26

<210> 307

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 307

aacgcagga tcttccagt cccttacatg aagactgaag atggg 45

<210> 308

<211> 1523

<212> DNA

<213> Homo sapiens

<400> 308

gagaggacga ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 50
cgagagccag ccctttccta acccaaccca acctagccca gtcccagccg 100
ccagcgctg tccctgtcac ggaccccagc gttaccatgc atcctgccgt 150
cttctatcc ttacccgacc tcagatgctc cttctgctc ctggtaactt 200
gggtttttac tcctgtaaca actgaaataa caagtcttgc tacagagaat 250
atagatgaaa ttttaaaca tgctgatgtt gctttagtaa attttatgc 300
tgactggtgt cgtttcagtc agatgttgca tccaattttt gaggaagctt 350
ccgatgtcat taaggaagaa tttccaatg aaaatcaagt agtgtttgcc 400
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 450
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 500
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggcaa 550
caaaaaagtg accccattca agaaattcgg gacttagcag aaatcaccac 600
tcttgatcgc agcaaaagaa atatcattgg atattttgag caaaaggact 650
cggacaacta tagagttttt gaacgagtag cgaatatatt gcgatgatgac 700
tgtgcctttc tttctgcatt tggggatgtt tcaaaaccgg aaagatatag 750
tggcgacaac ataatctaca aaccaccagg gcattctgct ccggatatgg 800
tgtacttggg agctatgaca aattttgatg tgacttaca ttggattcaa 850
gataaatgtg ttcctcttgt ccgagaaata acatttgaaa atggagagga 900
attgacagaa gaaggactgc cttttctcat actctttcac atgaaagaag 950
atacagaaaag tttagaaata ttccagaatg aagtagctcg gcaattaata 1000
agtgaaaaag gtacaataaa ctttttcat gccgattgtg acaaatttag 1050
acatcctctt ctgcacatac agaaaactcc agcagattgt cctgtaatcg 1100
ctattgacag ctttaggcat atgtatgtgt ttggagactt caaagatgta 1150
ttaattcctg gaaaactcaa gcaattcgta ttgacttac attctggaaa 1200
actgcacaga gaattccatc atggacctga cccaactgat acagccccag 1250

gagagcaagc ccaagatgta gcaagcagtc cacctgagag ctccttccag 1300
aaactagcac ccagtgaata taggtatact ctattgaggg atcgagatga 1350
gctttaaaaaa cttgaaaaaac agtttgtaag cctttcaaca gcagcatcaa 1400
cctacgtggt ggaaatagta aacctatatt ttcataattc tatgtgtatt 1450
tttattttga ataaacagaa agaaatttaa aaaaaaaaaa aaaaaaaaaa 1500
aaaaaaaaaa aaaaaaaaaa aaa 1523

<210> 309
<211> 406
<212> PRT
<213> Homo sapiens

<400> 309

Met	His	Pro	Ala	Val	Phe	Leu	Ser	Leu	Pro	Asp	Leu	Arg	Cys	Ser	1	5	10	15
Leu	Leu	Leu	Leu	Val	Thr	Trp	Val	Phe	Thr	Pro	Val	Thr	Thr	Glu	20	25	30	
Ile	Thr	Ser	Leu	Ala	Thr	Glu	Asn	Ile	Asp	Glu	Ile	Leu	Asn	Asn	35	40	45	
Ala	Asp	Val	Ala	Leu	Val	Asn	Phe	Tyr	Ala	Asp	Trp	Cys	Arg	Phe	50	55	60	
Ser	Gln	Met	Leu	His	Pro	Ile	Phe	Glu	Glu	Ala	Ser	Asp	Val	Ile	65	70	75	
Lys	Glu	Glu	Phe	Pro	Asn	Glu	Asn	Gln	Val	Val	Phe	Ala	Arg	Val	80	85	90	
Asp	Cys	Asp	Gln	His	Ser	Asp	Ile	Ala	Gln	Arg	Tyr	Arg	Ile	Ser	95	100	105	
Lys	Tyr	Pro	Thr	Leu	Lys	Leu	Phe	Arg	Asn	Gly	Met	Met	Met	Lys	110	115	120	
Arg	Glu	Tyr	Arg	Gly	Gln	Arg	Ser	Val	Lys	Ala	Leu	Ala	Asp	Tyr	125	130	135	
Ile	Arg	Gln	Gln	Lys	Ser	Asp	Pro	Ile	Gln	Glu	Ile	Arg	Asp	Leu	140	145	150	
Ala	Glu	Ile	Thr	Thr	Leu	Asp	Arg	Ser	Lys	Arg	Asn	Ile	Ile	Gly	155	160	165	
Tyr	Phe	Glu	Gln	Lys	Asp	Ser	Asp	Asn	Tyr	Arg	Val	Phe	Glu	Arg	170	175	180	
Val	Ala	Asn	Ile	Leu	His	Asp	Asp	Cys	Ala	Phe	Leu	Ser	Ala	Phe	185	190	195	

Gly	Asp	Val	Ser	Lys	Pro	Glu	Arg	Tyr	Ser	Gly	Asp	Asn	Ile	Ile	200	205	210
Tyr	Lys	Pro	Pro	Gly	His	Ser	Ala	Pro	Asp	Met	Val	Tyr	Leu	Gly	215	220	225
Ala	Met	Thr	Asn	Phe	Asp	Val	Thr	Tyr	Asn	Trp	Ile	Gln	Asp	Lys	230	235	240
Cys	Val	Pro	Leu	Val	Arg	Glu	Ile	Thr	Phe	Glu	Asn	Gly	Glu	Glu	245	250	255
Leu	Thr	Glu	Glu	Gly	Leu	Pro	Phe	Leu	Ile	Leu	Phe	His	Met	Lys	260	265	270
Glu	Asp	Thr	Glu	Ser	Leu	Glu	Ile	Phe	Gln	Asn	Glu	Val	Ala	Arg	275	280	285
Gln	Leu	Ile	Ser	Glu	Lys	Gly	Thr	Ile	Asn	Phe	Leu	His	Ala	Asp	290	295	300
Cys	Asp	Lys	Phe	Arg	His	Pro	Leu	Leu	His	Ile	Gln	Lys	Thr	Pro	305	310	315
Ala	Asp	Cys	Pro	Val	Ile	Ala	Ile	Asp	Ser	Phe	Arg	His	Met	Tyr	320	325	330
Val	Phe	Gly	Asp	Phe	Lys	Asp	Val	Leu	Ile	Pro	Gly	Lys	Leu	Lys	335	340	345
Gln	Phe	Val	Phe	Asp	Leu	His	Ser	Gly	Lys	Leu	His	Arg	Glu	Phe	350	355	360
His	His	Gly	Pro	Asp	Pro	Thr	Asp	Thr	Ala	Pro	Gly	Glu	Gln	Ala	365	370	375
Gln	Asp	Val	Ala	Ser	Ser	Pro	Pro	Glu	Ser	Ser	Phe	Gln	Lys	Leu	380	385	390
Ala	Pro	Ser	Glu	Tyr	Arg	Tyr	Thr	Leu	Leu	Arg	Asp	Arg	Asp	Glu	395	400	405

Leu

<210> 310
 <211> 182
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 36, 48
 <223> unknown base

<400> 310

attaaggaag aatttccaaa tgaaaatcaa gtagtnnttg ccagagtnga 50
ttgtgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100
caaccctcaa attgtttcgt aatgggatga tgatgaagag agaatacagg 150
ggtcagcgat cagtgaaagc attggcagat ta 182

<210> 311

<211> 598

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396

<223> unknown base

<400> 311

agaggcctct ctggaagttg tcccgggtgt tcgccgcngg agcccgggtc 50
gagaggacna ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 100
cggagcccag ccctttccta acccaaccca acctagcccn gtcccagccg 150
ccagcgcttg tccctgtcnc ggancccagc gtnaccatgc atcctgccgt 200
cttcctatcc ttacccgacc tcagatgctc ccttctgctc ctggtaactt 250
gggttttttac tcctgtaaca actgaaataa cnngtcttga tacnnagaat 300
atagatgaaa ttttaaacna tgctgatgtg gctttagtca atttttatgc 350
tgactggtgt cgtttcagtc agatgtggca tccaattttt gaggangctt 400
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 450
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 500
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 550
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggc 598

<210> 312

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 312

tgagaggcct ctctggaagt tg 22

<210> 313

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 313

gtcagcgatc agtgaaagc 19

<210> 314

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 314

ccagaatgaa gtagctcggc 20

<210> 315

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 315

ccgactcaaa atgcattgtc 20

<210> 316

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 316

catttggcag gaattgtcc 19

<210> 317

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 317

ggtgctatag gccaaagg 18

<210> 318

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 318

ctgtatctct gggctatgtc agag 24

<210> 319

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 319

ctacatataa tggcacatgt cagcc 25

<210> 320

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 320

cgtcttctta tccttaccgc acctcagatg ctcccttctg ctctg 46

<210> 321

<211> 1333

<212> DNA

<213> Homo sapiens

<400> 321

gcccacgcgt cegatggcgt tcacgttcgc ggccttctgc tacatgctgg 50

cgctgctgct cactgcgcgc ctcatcttct tcgccatttg gcacattata 100

gcatttgatg agctgaagac tgattacaag aatcctatag accagtgtaa 150

taccctgaat ccccttgtag tcccagagta cctcatccac gctttcttct 200

gtgtcatgtt tctttgtgca gcagagtggc ttacactggg tctcaatatg 250

cccctcttgg catatcatat ttggaggtat atgagtagac cagtgatgag 300

tggcccagga ctctatgacc ctacaaccat catgaatgca gatattctag 350

catattgtca gaaggaagga tggtgcaaat tagcttttta tcttctagca 400

tttttttact acctatatgg catgatctat gttttggtga gctcttagaa 450

caacacacag aagaattggc ccagtttaagt gcatgcaaaa agccaccaa 500

tgaagggatt ctatccagca agatcctgtc caagagtagc ctgtggaatc 550

tgatcagtta ctttaaaaaa tgactcctta ttttttaa atgtttccacat 600

ttttgcttgt ggaaagactg ttttcatatg ttatactcag ataaagattt 650
 taaatggtat tacgtataaa ttaatatataa atgattacct ctggtgttga 700
 caggtttgaa cttgcacttc ttaaggaaca gccataatcc tctgaatgat 750
 gcattaatta ctgactgtcc tagtacattg gaagcttttg tttataggaa 800
 cttgtagggc tcatttttgg ttcattgaaa cagtatctaa ttataaatta 850
 gctgtagata tcagggtgctt ctgatgaagt gaaaatgtat atctgactag 900
 tgggaaactt catgggtttc ctcactgtgc atgtcgatga ttatatatgg 950
 atacatttac aaaaataaaa agcgggaatt ttcccttcgc ttgaatatta 1000
 tccctgtata ttgcatgaat gagagatttc ccatatttcc atcagagtaa 1050
 taaatatact tgctttaatt cttaagcata agtaaacadg atataaaaaat 1100
 atatgctgaa ttacttgtga agaatgcatt taaagctatt ttaaagtgtg 1150
 ttttatttgt aagacattac ttattaagaa attggttatt atgcttactg 1200
 ttctaactcg gtggttaaagg tattcttaag aatttgcagg tactacagat 1250
 tttcaaaact gaatgagaga aaattgtata accatcctgc tgttccttta 1300
 gtgcaataca ataaaactct gaaattaaga ctc 1333

<210> 322
 <211> 144
 <212> PRT
 <213> Homo sapiens

<400> 322
 Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ala Leu Leu
 1 5 10 15
 Leu Thr Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala
 20 25 30
 Phe Asp Glu Leu Lys Thr Asp Tyr Lys Asn Pro Ile Asp Gln Cys
 35 40 45
 Asn Thr Leu Asn Pro Leu Val Leu Pro Glu Tyr Leu Ile His Ala
 50 55 60
 Phe Phe Cys Val Met Phe Leu Cys Ala Ala Glu Trp Leu Thr Leu
 65 70 75
 Gly Leu Asn Met Pro Leu Leu Ala Tyr His Ile Trp Arg Tyr Met
 80 85 90
 Ser Arg Pro Val Met Ser Gly Pro Gly Leu Tyr Asp Pro Thr Thr
 95 100 105

Ile Met Asn Ala Asp Ile Leu Ala Tyr Cys Gln Lys Glu Gly Trp
110 115 120

Cys Lys Leu Ala Phe Tyr Leu Leu Ala Phe Phe Tyr Tyr Leu Tyr
125 130 135

Gly Met Ile Tyr Val Leu Val Ser Ser
140

<210> 323

<211> 477

<212> DNA

<213> Homo sapiens

<400> 323

attatagcat ttgatgagct gaagactgat tacaagatcc tatagaccag 50
tgtaataccc tgaatcccct tgtactccca gagtaccta tccacgcttt 100
cttctgtgtc atgtttcttt gtgcagcaga gtggcttaca ctgggtctca 150
atatgcccct cttggcatat catatttggg ggtatatgag tagaccagtg 200
atgagtggcc caggactcta tgaccctaca accatcatga atgcagatat 250
tctagcatat tgtcagaagg aaggatgggtg caaattagct ttttatcttc 300
tagcattttt ttactaccta tatggcatga tctatgtttt ggtgagctct 350
tagaacaaca cacagaagaa ttggtccagt taagtgcagc caaaaagcca 400
ccaaatgaag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450
gaatctgata agttacttta aaaaatg 477

<210> 324

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 324

tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 325

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 325

caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 326
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 326
gtgcagcaga gtggcttaca 20

<210> 327
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 327
actggaccaa ttcttctgtg 20

<210> 328
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 328
gatattctag catattgtca gaaggaagga tgggtgcaaat tagct 45

<210> 329
<211> 1174
<212> DNA
<213> Homo sapiens

<400> 329
cggacgcgtg ggggaaaccc ttccgagaaa acagcaacaa gctgagctgc 50
tgtgacagag gggaacaaga tggcggcgcc gaaggggagc ctctgggtga 100
ggaccaact ggggctcccg ccgctgctgc tgctgaccat ggccttggcc 150
ggagggttcgg ggaccgcttc ggctgaagca tttgactcgg tcttgggtga 200
tacggcgtct tgccaccggg cctgtcagtt gacctacccc ttgcacacct 250
accctaagga agaggagttg tacgcatgtc agagaggttg caggctgttt 300
tcaatttgctc agtttgtgga tgatggaatt gacttaaata gaactaaatt 350
ggaatgtgaa tctgcatgta cagaagcata ttcccaatct gatgagcaat 400
atgcttgcca tcttgggttg cagaatcagc tgccattcgc tgaactgaga 450

caagaacaac ttatgtccct gatgccaaaa atgcacctac tctttcctct 500
 aactctggtg aggtcattct ggagtgcacat gatggactcc gcacagagct 550
 tcataacctc ttcattggact ttttatcttc aagccgatga cggaaaaata 600
 gttatattcc agtctaagcc agaaatccag tacgcaccac atttgagca 650
 ggagcctaca aatttgagag aatcatctct aagcaaatg tcctatctgc 700
 aaatgagaaa ttcacaagcg cacaggaatt ttcttgaaga tggagaaagt 750
 gatggctttt taagatgcct ctctcttaac tctgggtgga ttttaactac 800
 aactcttgtc ctctcggtga tggattgct ttggatttgt tgtgcaactg 850
 ttgctacagc tgtggagcag tatgttcct ctgagaagct gagtatctat 900
 ggtgacttgg agtttatgaa tgaacaaaag ctaaacagat atccagcttc 950
 ttctcttggtg gttgttagat ctaaaactga agatcatgaa gaagcagggc 1000
 ctctacctac aaaagtgaat cttgctcatt ctgaaattta agcatttttc 1050
 ttttaaaaga caagtgaat agacatctaa aattccactc ctcatagagc 1100
 ttttaaaatg gtttcattgg atataggcct taagaaatca ctataaaatg 1150
 caaataaagt tactcaaadc tgtg 1174

<210> 330

<211> 323

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ala	Pro	Lys	Gly	Ser	Leu	Trp	Val	Arg	Thr	Gln	Leu	Gly
1				5					10				15	
Leu	Pro	Pro	Leu	Leu	Leu	Leu	Thr	Met	Ala	Leu	Ala	Gly	Gly	Ser
			20						25				30	
Gly	Thr	Ala	Ser	Ala	Glu	Ala	Phe	Asp	Ser	Val	Leu	Gly	Asp	Thr
			35						40				45	
Ala	Ser	Cys	His	Arg	Ala	Cys	Gln	Leu	Thr	Tyr	Pro	Leu	His	Thr
			50						55				60	
Tyr	Pro	Lys	Glu	Glu	Glu	Leu	Tyr	Ala	Cys	Gln	Arg	Gly	Cys	Arg
			65						70				75	
Leu	Phe	Ser	Ile	Cys	Gln	Phe	Val	Asp	Asp	Gly	Ile	Asp	Leu	Asn
			80						85				90	
Arg	Thr	Lys	Leu	Glu	Cys	Glu	Ser	Ala	Cys	Thr	Glu	Ala	Tyr	Ser
			95						100				105	

Gln Ser Asp Glu Gln Tyr Ala Cys His Leu Gly Cys Gln Asn Gln	110	115	120
Leu Pro Phe Ala Glu Leu Arg Gln Glu Gln Leu Met Ser Leu Met	125	130	135
Pro Lys Met His Leu Leu Phe Pro Leu Thr Leu Val Arg Ser Phe	140	145	150
Trp Ser Asp Met Met Asp Ser Ala Gln Ser Phe Ile Thr Ser Ser	155	160	165
Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys Ile Val Ile Phe	170	175	180
Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu Glu Gln Glu	185	190	195
Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser Tyr Leu	200	205	210
Gln Met Arg Asn Ser Gln Ala His Arg Asn Phe Leu Glu Asp Gly	215	220	225
Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn Ser Gly Trp	230	235	240
Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu Leu Trp	245	250	255
Ile Cys Cys Ala Thr Val Ala Thr Ala Val Glu Gln Tyr Val Pro	260	265	270
Ser Glu Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe Met Asn Glu	275	280	285
Gln Lys Leu Asn Arg Tyr Pro Ala Ser Ser Leu Val Val Val Arg	290	295	300
Ser Lys Thr Glu Asp His Glu Glu Ala Gly Pro Leu Pro Thr Lys	305	310	315
Val Asn Leu Ala His Ser Glu Ile	320		

<210> 331

<211> 350

<212> DNA

<213> Homo sapiens

<400> 331

ttgggtgata cggcgtcttg ccaccgggcc tgtcagttga cctaccctt 50

gcacacctac cctaaggaag aggagttgta cgcattgtcag agaggttgca 100

ggctgttttc aatttgtcag tttgtggatg atggaattga cttaaattcga 150

actaaattgg aatgtgaatc tgcattgtaca gaagcatatt cccaatctga 200
tgagcaatat gcttgccatc ttggttgcca gaatcagctg ccattcgctg 250
aactgagaca agaacaactt atgtccctga tgccaaaaat gcacctactc 300
tttctcttaa ctctggtgag gtcattctgg agtgacatga tggactccgc 350

<210> 332
<211> 562
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 47
<223> unknown base

<400> 332
cacactggcc ggatctttta gagtcctttg accttgacca agggctcngga 50
aaacagcaac aagctgagct gctgtgacag agggacaag atggcggcgc 100
cgaaggagac ctttggttga ggaccaact ggggctcccg ccgctgctgc 150
tgctgaccat ggccttggcc ggagggttcg ggaccgcttc ggctgaagca 200
tttgactcgg tcttggttga tacggcgtct tgccaccggg cctgtcagtt 250
gacctacccc ttgcacacct accctaagga agaggagttg tacgcatgtc 300
agagaggttg caggctgttt tcaatttgtc agtttgtgga tgatggaatt 350
gacttaaata gaactaaatt ggaatgtgaa tctgcatgta cagaagcata 400
ttcccaatct gatgagcaat atgcttgcca tcttggttgc cagaatcagc 450
tgccattcgc tgaactgaga caagaacaac ttatgtccct gatgccaaaa 500
atgcacctac tctttctctt aactctggtg aggtcattct ggagtgcacat 550
gatggactcc gc 562

<210> 333
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 333
acaagctgag ctgctgtgac ag 22

<210> 334
<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 334

tgattctggc aaccaagatg gc 22

<210> 335

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 335

atggccttgg ccggagggtc ggggaccgct tcggctgaag 40

<210> 336

<211> 1885

<212> DNA

<213> Homo sapiens

<400> 336

gcgagggtggc gatcgctgag aggcaggagg gccgaggcgg gcctgggagg 50
cgggcccgag gtggggcgcc gctggggccg gcccgcacgg gttcatctg 100
agggcgcacg gcccgcgacc gagcgtgcgg actggcctcc caagcgtggg 150
gcgacaagct gccggagctg caatgggccg cggctgggga ttcttgtttg 200
gcctcctggg cgccgtgtgg ctgctcagct cgggccacgg agaggagcag 250
cccccggaga cagcggcaca gaggtgcttc tgccaggtta gtggttactt 300
ggatgattgt acctgtgatg ttgaaacat tgatagattt aataactaca 350
ggcttttccc aagactacaa aaacttcttg aaagtgacta ctttaggtat 400
tacaaggtaa acctgaagag gccgtgtcct ttctggaatg acatcagcca 450
gtgtggaaga agggactgtg ctgtcaaacc atgtcaatct gatgaagttc 500
ctgatggaat taaatctgcg agctacaagt attctgaaga agccaataat 550
ctcattgaag aatgtgaaca agctgaacga cttggagcag tggatgaatc 600
tctgagttag gaaacacaga aggtgttct tcagtggacc aagcatgatg 650
attcttcaga taacttctgt gaagctgatg acattcagtc ccctgaagct 700
gaatatgtag atttgcttct taatcctgag cgctacactg gttacaaggg 750
accagatgct tggaaaatat ggaatgtcat ctacgaagaa aactgtttta 800

agccacagac aattaaaaga cctttaaatc ctttggett c tggcaagg 850
 acaagtgaag agaacacttt ttacagttgg ctagaaggtc tctgtgtaga 900
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 tggggacaca acattacaga atttcaacag cgatttgatg gaattttgac 1050
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 tagaactaag ggctttatcc aaagtgttac cattcttcga gcgcccagat 1150
 tttcaactct ttactggaaa taaaattcag gatgaggaaa acaaaatggt 1200
 acttctggaa atacttcatg aaatcaagtc atttcctttg cattttgatg 1250
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 aaggagaatt atattgtttt aagtaaacac atttttaaaa attgtgttaa 1750
 gtctatgtat aatactactg tgagtaaaag taatacttta ataatgtgg 1800
 acaaatttta aagtttaata ttgaataaaa ggaggattat caaattaaaa 1850
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1885

<210> 337

<211> 468

<212> PRT

<213> Homo sapiens

<400> 337

Met	Gly	Arg	Gly	Trp	Gly	Phe	Leu	Phe	Gly	Leu	Leu	Gly	Ala	Val
1				5					10				15	

Trp	Leu	Leu	Ser	Ser	Gly	His	Gly	Glu	Glu	Gln	Pro	Pro	Glu	Thr
			20					25					30	

Ala	Ala	Gln	Arg	Cys	Phe	Cys	Gln	Val	Ser	Gly	Tyr	Leu	Asp	Asp		35	40	45
Cys	Thr	Cys	Asp	Val	Glu	Thr	Ile	Asp	Arg	Phe	Asn	Asn	Tyr	Arg		50	55	60
Leu	Phe	Pro	Arg	Leu	Gln	Lys	Leu	Leu	Glu	Ser	Asp	Tyr	Phe	Arg		65	70	75
Tyr	Tyr	Lys	Val	Asn	Leu	Lys	Arg	Pro	Cys	Pro	Phe	Trp	Asn	Asp		80	85	90
Ile	Ser	Gln	Cys	Gly	Arg	Arg	Asp	Cys	Ala	Val	Lys	Pro	Cys	Gln		95	100	105
Ser	Asp	Glu	Val	Pro	Asp	Gly	Ile	Lys	Ser	Ala	Ser	Tyr	Lys	Tyr		110	115	120
Ser	Glu	Glu	Ala	Asn	Asn	Leu	Ile	Glu	Glu	Cys	Glu	Gln	Ala	Glu		125	130	135
Arg	Leu	Gly	Ala	Val	Asp	Glu	Ser	Leu	Ser	Glu	Glu	Thr	Gln	Lys		140	145	150
Ala	Val	Leu	Gln	Trp	Thr	Lys	His	Asp	Asp	Ser	Ser	Asp	Asn	Phe		155	160	165
Cys	Glu	Ala	Asp	Asp	Ile	Gln	Ser	Pro	Glu	Ala	Glu	Tyr	Val	Asp		170	175	180
Leu	Leu	Leu	Asn	Pro	Glu	Arg	Tyr	Thr	Gly	Tyr	Lys	Gly	Pro	Asp		185	190	195
Ala	Trp	Lys	Ile	Trp	Asn	Val	Ile	Tyr	Glu	Glu	Asn	Cys	Phe	Lys		200	205	210
Pro	Gln	Thr	Ile	Lys	Arg	Pro	Leu	Asn	Pro	Leu	Ala	Ser	Gly	Gln		215	220	225
Gly	Thr	Ser	Glu	Glu	Asn	Thr	Phe	Tyr	Ser	Trp	Leu	Glu	Gly	Leu		230	235	240
Cys	Val	Glu	Lys	Arg	Ala	Phe	Tyr	Arg	Leu	Ile	Ser	Gly	Leu	His		245	250	255
Ala	Ser	Ile	Asn	Val	His	Leu	Ser	Ala	Arg	Tyr	Leu	Leu	Gln	Glu		260	265	270
Thr	Trp	Leu	Glu	Lys	Lys	Trp	Gly	His	Asn	Ile	Thr	Glu	Phe	Gln		275	280	285
Gln	Arg	Phe	Asp	Gly	Ile	Leu	Thr	Glu	Gly	Glu	Gly	Pro	Arg	Arg		290	295	300
Leu	Lys	Asn	Leu	Tyr	Phe	Leu	Tyr	Leu	Ile	Glu	Leu	Arg	Ala	Leu		305	310	315

Ser	Lys	Val	Leu	Pro	Phe	Phe	Glu	Arg	Pro	Asp	Phe	Gln	Leu	Phe	320	325	330
Thr	Gly	Asn	Lys	Ile	Gln	Asp	Glu	Glu	Asn	Lys	Met	Leu	Leu	Leu	335	340	345
Glu	Ile	Leu	His	Glu	Ile	Lys	Ser	Phe	Pro	Leu	His	Phe	Asp	Glu	350	355	360
Asn	Ser	Phe	Phe	Ala	Gly	Asp	Lys	Lys	Glu	Ala	His	Lys	Leu	Lys	365	370	375
Glu	Asp	Phe	Arg	Leu	His	Phe	Arg	Asn	Ile	Ser	Arg	Ile	Met	Asp	380	385	390
Cys	Val	Gly	Cys	Phe	Lys	Cys	Arg	Leu	Trp	Gly	Lys	Leu	Gln	Thr	395	400	405
Gln	Gly	Leu	Gly	Thr	Ala	Leu	Lys	Ile	Leu	Phe	Ser	Glu	Lys	Leu	410	415	420
Ile	Ala	Asn	Met	Pro	Glu	Ser	Gly	Pro	Ser	Tyr	Glu	Phe	His	Leu	425	430	435
Thr	Arg	Gln	Glu	Ile	Val	Ser	Leu	Phe	Asn	Ala	Phe	Gly	Arg	Ile	440	445	450
Ser	Thr	Ser	Val	Lys	Glu	Leu	Glu	Asn	Phe	Arg	Asn	Leu	Leu	Gln	455	460	465

Asn Ile His

<210> 338
 <211> 507
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 101, 263, 376, 397, 426
 <223> unknown base

<400> 338
 gctggaaata tggatgtcat ctacgagaaa ctgttttaag ccacagacaa 50
 ttaaaagacc tttaaactct ttggcttctg gtcaaggac aagtgaagag 100
 nacacttttt acagttggct agaaggtctc tgtgtagaaa aaagagcatt 150
 ctacagactt atatctggcc tacatgcaag cattaatgtg catttgagtg 200
 caagatatct tttaacaagag acctgggttag aaaagaaatg gggacacaac 250
 attacagaat ttnaacagcg atttgatgga attttgactg aaggagaagg 300
 tccaagaagg cttaagaact tgtattttct ctacttaata gaactaaggg 350

ctttatccaa agtgttacca ttcttngagc gccagattt tcaactnttt 400
actggaaata aaattcagga tgaggnaaac aaaatgttac ttttggaat 450
acttcatgaa atcaagtcatt ttcctttgca ttttgatgag aattcatttt 500
tttgctg 507

<210> 339
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 339
aagctgccgg agctgcaatg 20

<210> 340
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 340
ttgcttctta atcctgagcg c 21

<210> 341
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 341
aaaggaggac tttcgactgc 20

<210> 342
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 342
agagattcat ccactgctcc aagtcg 26

<210> 343
<211> 25
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 343

tgtccagaaa caggcacata tcagc 25

<210> 344

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

agacagcggc acagaggtgc ttctgccagg ttagtggtta cttggatgat 50

<210> 345

<211> 1486

<212> DNA

<213> Homo sapiens

<400> 345

cggacgcgtg ggcggacgcg tgggcggacg cgtgggttgg gagggggcag 50
gatgggaggg aaagtgaaga aaacagaaaa ggagagggac agaggccaga 100
ggacttctca tactggacag aaaccgatca ggcattggaac tccccttcgt 150
cactcacctg ttcttgcccc tgggtgttctt gacaggtctc tgctccccct 200
ttaacctgga tgaacatcac ccacgcctat tcccagggcc accagaagct 250
gaatttggat acagtgtctt acaacatgtt gggggtggac agcgatggat 300
gctggtgggc gccccctggg atgggccttc aggcgaccgg aggggggacg 350
tttatcgctg ccctgtaggg ggggccaca atgccccatg tgccaagggc 400
cacttaggtg actaccaact gggaaattca tctcatcctg ctgtgaatat 450
gcacctgggg atgtctctgt tagagacaga tggatgatgg ggattcatgg 500
tgagctaagg agaggttggg ggcagtgtct ctgaaggtcc ataaaagaaa 550
aaagagaagt gtggttaaggg aaaatggtct gtgtggaggg gtcaaggagt 600
taaaaaccct agaaagcaaa aggtaggtaa tgtcaggag tagtcttcat 650
gcctccttca actgggagca tgttctgagg gtgccctccc aagcctggga 700
gtaactatth ccccatccc caggcctgtg cccctctctg gtctcgtgct 750
tgtggcagct ctgtcttcag ttctgggata tgtgccctg tggtatgctc 800
attccagcct cagggaagcc tggcaccac tgcccaacgt gagccagagg 850

aaggctgagt acttggttcc cagaaggaga tactgggtgg gaaaaagatg 900
gggcaaagcg gtatgatgcc tggcaaaggg cctgcatggc taccctcatt 950
gctacctaata gtgcttgcaa aagctccatg tttcctaaca gattcagact 1000
cctggccagg tgtggtggcc cacacctgta attctagcac tttgggaggc 1050
caaggtgggc agatcacttg aggtcaggag ttcaagacca gcctggccaa 1100
catggtgaaa ctccatctct actaaaaaaaa aaaaaataca aaaattagct 1150
gggtgcgcta gtgcatgcct gtaatctcat ctactcggga ggctaagaca 1200
ggagactctc acttcaaccc aggaggtgga ggttgcggtg agccaagatt 1250
gtgcctctgc actctagcgt gggtgacaga gtaagcgaga ctccatctca 1300
aaaataataa taataataat tcagactcct tatcaggagt ccatgatctg 1350
gcctggcaca gtaactcatg cctgtaatcc caacattttg ggaggccaac 1400
gcaggaggat tgcttgaggt ctggaggttt gagaccagcc tgggcaacat 1450
agaaagaccc catctctaaa taaatgtttt aaaaat 1486

<210> 346
<211> 124
<212> PRT
<213> Homo sapiens

<400> 346
Met Glu Leu Pro Phe Val Thr His Leu Phe Leu Pro Leu Val Phe
1 5 10 15
Leu Thr Gly Leu Cys Ser Pro Phe Asn Leu Asp Glu His His Pro
20 25 30
Arg Leu Phe Pro Gly Pro Pro Glu Ala Glu Phe Gly Tyr Ser Val
35 40 45
Leu Gln His Val Gly Gly Gly Gln Arg Trp Met Leu Val Gly Ala
50 55 60
Pro Trp Asp Gly Pro Ser Gly Asp Arg Arg Gly Asp Val Tyr Arg
65 70 75
Cys Pro Val Gly Gly Ala His Asn Ala Pro Cys Ala Lys Gly His
80 85 90
Leu Gly Asp Tyr Gln Leu Gly Asn Ser Ser His Pro Ala Val Asn
95 100 105
Met His Leu Gly Met Ser Leu Leu Glu Thr Asp Gly Asp Gly Gly
110 115 120

Phe Met Val Ser

<210> 347
<211> 509
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 22
<223> unknown base

<400> 347
cacagttccc caccatcact cntcccatc cttccaactt tatttttagc 50
ttgccattgg gagggggcag gatgggaggg aaagtgaaga aaacagaaaa 100
ggagagggac agaggccaga ggacttctca tactggacag aaaccgatca 150
ggcatggaac tccccttcgt cactcacctg ttcttgcccc tgggtgttcct 200
gacaggtctc tgctccccct ttaacctgga tgaacatcac ccacgcctat 250
tcccagggcc accagaagct gaatttggat acagtgtctt acaacatggt 300
gggggtggac agcgatggat gctgggtgggc gcccctggg atgggccttc 350
aggcgaccgg aggggggacg tttatcgctg ccctgtaggg gggggccaca 400
atgccccatg tgccaagggc cacttaggtg actaccaact gggaaattca 450
tctcatcctg ctgtgaatat gcacctgggg atgtctctgt tagagacaga 500
tggtgatgg 509

<210> 348
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 348
agggacagag gccagaggac ttc 23

<210> 349
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 349
caggtgcata ttcacagcag gatg 24

<210> 350
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 350
ggaactcccc ttcgtcactc acctgttctt gcccctggtg ttcct 45

<210> 351
<211> 2056
<212> DNA
<213> Homo sapiens

<400> 351
aaagttacat tttctctgga actctcctag gccactccct gctgatgcaa 50
catctggggtt tgggcagaaa ggagggtgct tcggagcccg ccctttctga 100
gcttcctggg ccggctctag aacaattcag gcttcgctgc gactcagacc 150
tcagctccaa catatgcatt ctgaagaaag atggctgaga tggacagaat 200
gctttatttt ggaaagaaac aatgttctag gtcaaactga gtctacaaa 250
tgcagacttt cacaatgggt ctagaagaaa tctggacaag tcttttcatg 300
tggtttttct acgcattgat tccatgtttg ctacacagatg aagtggccat 350
tctgcctgcc cctcagaacc tctctgtact ctcaaccaac atgaagcatc 400
tcttgatgtg gagcccagtg atcgcgctg gagaaacagt gtactattct 450
gtcgaatacc agggggagta cgagagcctg tacacgagcc acatctggat 500
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atgacatcac ggccactgtg ccatacaacc ttcgtgtcag ggccacattg 600
ggctcacaga cctcagcctg gagcatcctg aagcatccct ttaatagaaa 650
ctcaaccatc cttacccgac ctgggatgga gatcaccaaa gatggcttcc 700
acctgggttat tgagctggag gacctggggc ccagtttga gttccttgtg 750
gcctactgga ggaggagacc tggtgccgag gaacatgtca aaatggtgag 800
gagtgggggt attccagtgc acctagaaac catggagcca ggggctgcat 850
actgtgtgaa ggcccagaca ttcgtgaagg ccattgggag gtacagcgcc 900
ttcagccaga cagaatgtgt ggagggtgcaa ggagaggcca ttcccctggt 950
actggccctg tttgcctttg ttggcttcat gctgacctt gtggtcgtgc 1000

cactgttcgt ctggaaaatg ggccggctgc tccagtactc ctgttgcccc 1050
 gtgggtggccc tcccagacac cttgaaaata accaattcac cccagaagtt 1100
 aatcagctgc agaagggagg aggtggatgc ctgtgccacg gctgtgatgt 1150
 ctcttgagga actcctcagg gcctggatct cataggtttg cggaagggcc 1200
 caggtgaagc cgagaacctg gtctgcatga catggaaacc atgaggggac 1250
 aagttgtgtt tctgttttcc gccacggaca agggatgaga gaagtaggaa 1300
 gagcctgttg tctacaagtc tagaagcaac catcagaggc aggggtggtt 1350
 gtctaacaga aactgactg aggccttaggg gatgtgacct ctagactggg 1400
 ggctgccact tgctggctga gcaacctgg gaaaagtgc ttcacccctt 1450
 cggtcctaag ttttctcacc tgtaatgggg gaattaccta cacacctgct 1500
 aaacacacac acacagagtc tctctctata tatacacacg tacacataaa 1550
 tacaccacgc acttgcaagg ctagagggaa actggtgaca ctctacagtc 1600
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 taatccttga gagaaaagga atcatgggag caatggtgtt gagttcactt 1750
 caagcccaat gccggtgcag aggggaatgg cttagcgagc tctacagtag 1800
 gtgacctgga ggaaggtcac agccacactg aaaatgggat gtgcatgaac 1850
 acggaggatc catgaactac tgtaaagtgt tgacagtgtg tgcacactgc 1900
 agacagcagg tgaaatgtat gtgtgcaatg cgacgagaat gcagaagtca 1950
 gtaacatgtg catgtttgtt gtgtctcttt tttctgttgg taaagtacag 2000
 aattcagcaa ataaaaaggg ccacctggc caaaagcggg aaaaaaaaaa 2050
 aaaaaa 2056

<210> 352

<211> 311

<212> PRT

<213> Homo sapiens

<400> 352

Met	Gln	Thr	Phe	Thr	Met	Val	Leu	Glu	Glu	Ile	Trp	Thr	Ser	Leu
1				5						10				15

Phe	Met	Trp	Phe	Phe	Tyr	Ala	Leu	Ile	Pro	Cys	Leu	Leu	Thr	Asp
				20					25					30

Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser	35	40	45
Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro	50	55	60
Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu	65	70	75
Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser	80	85	90
Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala	95	100	105
Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln	110	115	120
Thr Ser Ala Trp Ser Ile Leu Lys His Pro Phe Asn Arg Asn Ser	125	130	135
Thr Ile Leu Thr Arg Pro Gly Met Glu Ile Thr Lys Asp Gly Phe	140	145	150
His Leu Val Ile Glu Leu Glu Asp Leu Gly Pro Gln Phe Glu Phe	155	160	165
Leu Val Ala Tyr Trp Arg Arg Glu Pro Gly Ala Glu Glu His Val	170	175	180
Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu Glu Thr Met	185	190	195
Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe Val Lys	200	205	210
Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val Glu	215	220	225
Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe	230	235	240
Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp	245	250	255
Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val	260	265	270
Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile	275	280	285
Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met	290	295	300
Ser Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser	305	310	

<210> 353
<211> 864
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 654, 711, 748, 827
<223> unknown base

<400> 353
tcctgctgat gcacatctgg gtttggcaaa aggaggttgc ttcgagccgc 50
cctttctagc ttcttgccg gctctagaac aattcaggct tcgctgcgac 100
tagacctcag ctccaacata tgcatctga agaaagatgg ctgagatgac 150
agaatgcttt attttgaaa gaaacaatgt tctaggtcaa actgagtcta 200
ccaaatgcag actttcacia tggttctaga agaaatctgg acaagtcttt 250
tcatgtggtt tttctacgca ttgattccat gtttgctcac agatgaagtg 300
gccattctgc ctgcccctca gaacctctct gtactctcaa ccaacatgaa 350
gcatctcttg atgtggagcc cagtgatcgc gcctggagaa acagtgtact 400
attctgtcga ataccagggg gactacgaga gcctgtacac gagccacatc 450
tggatcccca gcagctggtg ctactcact gaaggctcctg agtgtgatgt 500
cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggcca 550
cattgggctc acagacctca gcctggagca tcctgaagca tccctttaat 600
agaaactcaa ccatccttac ccgacctggg atggagatca ccaaagatgg 650
cttncacctg gttattgagc tggaggacct ggggccccag tttgagttcc 700
ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750
gaacccttg cggccgctgg ggtatctctc gagaaaagag aggcccaata 800
tgaccacat actcaatatg gacgaantgc tattgtccac ctgtttgagt 850
ggcgctgggt tgat 864

<210> 354
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 354
aggcttcgct gcgactagac ctc 23

<210> 355
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 355
ccaggtcggg taaggatggt tgag 24

<210> 356
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 356
tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 357
<211> 1670
<212> DNA
<213> Homo sapiens

<400> 357
cccacgcgtc cgcccacgcg tccgaggac aagagagaag agagactgaa 50
acaggagaaa gaggcaggag aggaggaggt ggggagagca cgaagctgga 100
ggccgacact gagggagggc gggaggaggt gaagaaggag agaggggaga 150
agaggcagga gctggaaagg agagagggag gaggaggagg agatgcggga 200
tgagagacctg gagttaggtg gcttgggaga gcttaatgaa aagagaacgg 250
agaggaggtg tgggttagga accaagaggt agccctgtgg gcagcagaag 300
gctgagagga gtaggaagat caggagctag agggagactg gagggttccg 350
ggaaaagagc agaggaaaaga ggaaagacac agagagacgg gagagagaag 400
aagagtgggt ttgaagggcg gatctcagtc cctggctgct ttggcatttg 450
gggaactggg actccctgtg gggaggagag gaaagctgga agtcctggag 500
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gcgttgggca ggggtccctc ggaggcctcc tggggatggg ggctgcagct 600
cgtctgagcg cccctcgagc gctggtactc tgggctgcac tgggggcagc 650
agctcacatc ggaccagcac ctgacccga ggactggtgg agctacaagg 700

ataatctcca gggaaacttc gtgccagggc ctcctttctg gggcctggtg 750
 aatgcagcgt ggagtctgtg tgctgtgggg aagcggcaga gccccgtgga 800
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 tgggtgtccc catggtcgt gagactcccc ttcgaggatt gcaccgccc 1600
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<210> 358

<211> 328

<212> PRT

<213> Homo sapiens

<400> 358

Met	Gly	Ala	Ala	Ala	Arg	Leu	Ser	Ala	Pro	Arg	Ala	Leu	Val	Leu
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Trp	Ala	Ala	Leu	Gly	Ala	Ala	Ala	His	Ile	Gly	Pro	Ala	Pro	Asp
				20					25					30

Pro	Glu	Asp	Trp	Trp	Ser	Tyr	Lys	Asp	Asn	Leu	Gln	Gly	Asn	Phe
				35					40					45

Val	Pro	Gly	Pro	Pro	Phe	Trp	Gly	Leu	Val	Asn	Ala	Ala	Trp	Ser
				50					55					60

Leu	Cys	Ala	Val	Gly	Lys	Arg	Gln	Ser	Pro	Val	Asp	Val	Glu	Leu	
				65					70					75	
Lys	Arg	Val	Leu	Tyr	Asp	Pro	Phe	Leu	Pro	Pro	Leu	Arg	Leu	Ser	
				80					85					90	
Thr	Gly	Gly	Glu	Lys	Leu	Arg	Gly	Thr	Leu	Tyr	Asn	Thr	Gly	Arg	
				95					100					105	
His	Val	Ser	Phe	Leu	Pro	Ala	Pro	Arg	Pro	Val	Val	Asn	Val	Ser	
				110					115					120	
Gly	Gly	Pro	Leu	Leu	Tyr	Ser	His	Arg	Leu	Ser	Glu	Leu	Arg	Leu	
				125					130					135	
Leu	Phe	Gly	Ala	Arg	Asp	Gly	Ala	Gly	Ser	Glu	His	Gln	Ile	Asn	
				140					145					150	
His	Gln	Gly	Phe	Ser	Ala	Glu	Val	Gln	Leu	Ile	His	Phe	Asn	Gln	
				155					160					165	
Glu	Leu	Tyr	Gly	Asn	Phe	Ser	Ala	Ala	Ser	Arg	Gly	Pro	Asn	Gly	
				170					175					180	
Leu	Ala	Ile	Leu	Ser	Leu	Phe	Val	Asn	Val	Ala	Ser	Thr	Ser	Asn	
				185					190					195	
Pro	Phe	Leu	Ser	Arg	Leu	Leu	Asn	Arg	Asp	Thr	Ile	Thr	Arg	Ile	
				200					205					210	
Ser	Tyr	Lys	Asn	Asp	Ala	Tyr	Phe	Leu	Gln	Asp	Leu	Ser	Leu	Glu	
				215					220					225	
Leu	Leu	Phe	Pro	Glu	Ser	Phe	Gly	Phe	Ile	Thr	Tyr	Gln	Gly	Ser	
				230					235					240	
Leu	Ser	Thr	Pro	Pro	Cys	Ser	Glu	Thr	Val	Thr	Trp	Ile	Leu	Ile	
				245					250					255	
Asp	Arg	Ala	Leu	Asn	Ile	Thr	Ser	Leu	Gln	Met	His	Ser	Leu	Arg	
				260					265					270	
Leu	Leu	Ser	Gln	Asn	Pro	Pro	Ser	Gln	Ile	Phe	Gln	Ser	Leu	Ser	
				275					280					285	
Gly	Asn	Ser	Arg	Pro	Leu	Gln	Pro	Leu	Ala	His	Arg	Ala	Leu	Arg	
				290					295					300	
Gly	Asn	Arg	Asp	Pro	Arg	His	Pro	Glu	Arg	Arg	Cys	Arg	Gly	Pro	
				305					310					315	
Asn	Tyr	Arg	Leu	His	Val	Asp	Gly	Val	Pro	His	Gly	Arg			
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<210> 359

<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 359
tctgctgagg tgcagctcat tcac 24

<210> 360
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 360
gaggctctgg aagatctgag atgg 24

<210> 361
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 361
gcctctttgt caacgttgcc agtacctcta acccattcct cagtcgcctc 50

<210> 362
<211> 3038
<212> DNA
<213> Homo sapiens

<400> 362
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gcagctccct tcccaccca actgcaggtc taattttgga cgctttgcct 200
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ctgcagtcag caccacgtc gccccggac gctcggtgct caggcccttc 300
gcgagcgggg ctctccgtct gcggtccctt gtgaaggctc tgggcggctg 350
cagaggccgg ccgtccggtt tggctcacct ctcccaggaa acttcacact 400
ggagagccaa aaggagtgga agagcctgtc ttggagattt tcctggggaa 450
atcctgaggt cattcattat gaagtgtacc gcgcgggagt ggctcagagt 500

aaccacagtg ctgttcatgg ctagagcaat tccagccatg gtggttccca 550
atgccacttt attggagaaa cttttggaaa aatacatgga tgaggatggt 600
gagtgggtgga tagccaaaca acgagggaaa agggccatca cagacaatga 650
catgcagagt attttggacc ttcataataa attacgaagt caggtgtatc 700
caacagcctc taatatggag tatatgacat gggatgtaga gctggaaaga 750
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gtagcagaaa tgaagtcata agcgcacagc aaatgtcca aattgtttct 1350
tgtgaagtaa gattaagaga tcagtgcata ggaacaacct gcaataggta 1400
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 taaatcttga taaacaaagt ctataaaata aaacatggga cattagcttt 2150
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 aaatgtattg tgctttgata ctaaaaatct gtaaaatggt agttttggta 2950
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 taaacattaa aattaatcat gtttcaaaaa aaaaaaaaa 3038

<210> 363

<211> 500

<212> PRT

<213> Homo sapiens

<400> 363

Met	Lys	Cys	Thr	Ala	Arg	Glu	Trp	Leu	Arg	Val	Thr	Thr	Val	Leu
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Phe	Met	Ala	Arg	Ala	Ile	Pro	Ala	Met	Val	Val	Pro	Asn	Ala	Thr
				20					25					30

Leu	Leu	Glu	Lys	Leu	Leu	Glu	Lys	Tyr	Met	Asp	Glu	Asp	Gly	Glu			
				35					40					45			
Trp	Trp	Ile	Ala	Lys	Gln	Arg	Gly	Lys	Arg	Ala	Ile	Thr	Asp	Asn			
				50					55					60			
Asp	Met	Gln	Ser	Ile	Leu	Asp	Leu	His	Asn	Lys	Leu	Arg	Ser	Gln			
				65					70					75			
Val	Tyr	Pro	Thr	Ala	Ser	Asn	Met	Glu	Tyr	Met	Thr	Trp	Asp	Val			
				80					85					90			
Glu	Leu	Glu	Arg	Ser	Ala	Glu	Ser	Trp	Ala	Glu	Ser	Cys	Leu	Trp			
				95					100					105			
Glu	His	Gly	Pro	Ala	Ser	Leu	Leu	Pro	Ser	Ile	Gly	Gln	Asn	Leu			
				110					115					120			
Gly	Ala	His	Trp	Gly	Arg	Tyr	Arg	Pro	Pro	Thr	Phe	His	Val	Gln			
				125					130					135			
Ser	Trp	Tyr	Asp	Glu	Val	Lys	Asp	Phe	Ser	Tyr	Pro	Tyr	Glu	His			
				140					145					150			
Glu	Cys	Asn	Pro	Tyr	Cys	Pro	Phe	Arg	Cys	Ser	Gly	Pro	Val	Cys			
				155					160					165			
Thr	His	Tyr	Thr	Gln	Val	Val	Trp	Ala	Thr	Ser	Asn	Arg	Ile	Gly			
				170					175					180			
Cys	Ala	Ile	Asn	Leu	Cys	His	Asn	Met	Asn	Ile	Trp	Gly	Gln	Ile			
				185					190					195			
Trp	Pro	Lys	Ala	Val	Tyr	Leu	Val	Cys	Asn	Tyr	Ser	Pro	Lys	Gly			
				200					205					210			
Asn	Trp	Trp	Gly	His	Ala	Pro	Tyr	Lys	His	Gly	Arg	Pro	Cys	Ser			
				215					220					225			
Ala	Cys	Pro	Pro	Ser	Phe	Gly	Gly	Gly	Cys	Arg	Glu	Asn	Leu	Cys			
				230					235					240			
Tyr	Lys	Glu	Gly	Ser	Asp	Arg	Tyr	Tyr	Pro	Pro	Arg	Glu	Glu	Glu			
				245					250					255			
Thr	Asn	Glu	Ile	Glu	Arg	Gln	Gln	Ser	Gln	Val	His	Asp	Thr	His			
				260					265					270			
Val	Arg	Thr	Arg	Ser	Asp	Asp	Ser	Ser	Arg	Asn	Glu	Val	Ile	Ser			
				275					280					285			
Ala	Gln	Gln	Met	Ser	Gln	Ile	Val	Ser	Cys	Glu	Val	Arg	Leu	Arg			
				290					295					300			
Asp	Gln	Cys	Lys	Gly	Thr	Thr	Cys	Asn	Arg	Tyr	Glu	Cys	Pro	Ala			
				305					310					315			

Gly Cys Leu Asp Ser Lys Ala Lys Val Ile Gly Ser Val His Tyr	320	325	330
Glu Met Gln Ser Ser Ile Cys Arg Ala Ala Ile His Tyr Gly Ile	335	340	345
Ile Asp Asn Asp Gly Gly Trp Val Asp Ile Thr Arg Gln Gly Arg	350	355	360
Lys His Tyr Phe Ile Lys Ser Asn Arg Asn Gly Ile Gln Thr Ile	365	370	375
Gly Lys Tyr Gln Ser Ala Asn Ser Phe Thr Val Ser Lys Val Thr	380	385	390
Val Gln Ala Val Thr Cys Glu Thr Thr Val Glu Gln Leu Cys Pro	395	400	405
Phe His Lys Pro Ala Ser His Cys Pro Arg Val Tyr Cys Pro Arg	410	415	420
Asn Cys Met Gln Ala Asn Pro His Tyr Ala Arg Val Ile Gly Thr	425	430	435
Arg Val Tyr Ser Asp Leu Ser Ser Ile Cys Arg Ala Ala Val His	440	445	450
Ala Gly Val Val Arg Asn His Gly Gly Tyr Val Asp Val Met Pro	455	460	465
Val Asp Lys Arg Lys Thr Tyr Ile Ala Ser Phe Gln Asn Gly Ile	470	475	480
Phe Ser Glu Ser Leu Gln Asn Pro Pro Gly Gly Lys Ala Phe Arg	485	490	495
Val Phe Ala Val Val	500		

<210> 364

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 364

ggacagaatt tgggagcaca ctgg 24

<210> 365

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 365
ccaagagtat actgtcctcg 20

<210> 366
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 366
agcacagatt ttctctacag ccccc 25

<210> 367
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 367
aaccactcca gcatgtactg ctgc 24

<210> 368
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 368
ccattcaggt gttctggccc tgtatgtaca cattatacac aggtcgtgtg 50

<210> 369
<211> 1685
<212> DNA
<213> Homo sapiens

<400> 369
gcggagacaa gcgcagagcg cagcgcacgg ccacagacag ccctgggcat 50
ccaccgacgg cgcagccgga gccagcagag ccggaaggcg cgccccgggc 100
agagaaagcc gagcagagct ggggtggcgtc tccggggcgc cgctccgacg 150
ggccagcgcc ctccccatgt ccctgctccc acgccgcgcc cctccggtca 200
gcatgaggct cctggcgggc gcgctgctcc tgctgctgct ggcgctgtac 250
accgcgcgtg tggacgggtc caaatgcaag tgctcccga agggacccaa 300
gatccgctac agcgacgtga agaagctgga aatgaagcca aagtaccgcg 350

actgcgagga gaagatgggtt atcatcacca ccaagagcgt gtccagggtac 400
 cgagggtcagg agcactgcct gcacccaag ctgcagagca ccaagcgctt 450
 catcaagtgg tacaacgcct ggaacgagaa gcgcagggtc tacgaagaat 500
 agggtgaaaa acctcagaag ggaaaaactcc aaaccagttg ggagacttgt 550
 gcaaaggact ttgcagatta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 600
 aaaaaaaaaa aaagcctttc tttctcacag gcataagaca caaattatat 650
 attgttatga agcacttttt accaacggtc agtttttaca ttttatagct 700
 gcgtgcgaaa ggcttcaga tgggagaccc atctctcttg tgctccagac 750
 ttcatcacag gctgcttttt atcaaaaagg ggaaaactca tgcttttcct 800
 ttttaaaaaa tgcttttttg tatttgtcca tacgtcacta tacatctgag 850
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 cagtgttgct ccattcctag ctgggaagc ttccgcttag aggtcctggc 950
 gcctcggcac agctgccacg ggctctcctg ggcttatggc cggtcacagc 1000
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 ctctctgcat ctgttctctg aggaactcaa gtttggttgc cagaaaaatg 1100
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 agatcctgtg atggcgagac aaatgatcct taaagaaggt gtggggctct 1200
 tccaacctg aggatttctg aaagggtcac aggttcaata tttaatgctt 1250
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 cttaaaaata tatgaatata tgcgcaatac acagctacag acacacattc 1350
 tgttgacaag ggaaaacctt caaagcatgt ttcttttcct caccacaaca 1400
 gaacatgcag tactaaagca atatatttgt gattcccat gtaattcttc 1450
 aatgttaaac agtgcagtcc tctttcgaaa gctaagatga ccatgcgccc 1500
 tttcctctgt acatataccc ttaagaacgc cccctccaca cactgcccc 1550
 cagtatatgc cgcattgtac tgctgtgtta tatgctatgt acatgtcaga 1600
 aaccattagc attgcatgca ggtttcatat tctttctaag atggaaagta 1650
 ataaaatata tttgaaatgt aaaaaaaaaa aaaaa 1685

<210> 370

<211> 111

<212> PRT

<213> Homo sapiens

<400> 370

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Leu	Ala	Ala	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Leu	Tyr	Thr	Ala	
				20				25						30	
Arg	Val	Asp	Gly	Ser	Lys	Cys	Lys	Cys	Ser	Arg	Lys	Gly	Pro	Lys	
				35				40						45	
Ile	Arg	Tyr	Ser	Asp	Val	Lys	Lys	Leu	Glu	Met	Lys	Pro	Lys	Tyr	
				50				55						60	
Pro	His	Cys	Glu	Glu	Lys	Met	Val	Ile	Ile	Thr	Thr	Lys	Ser	Val	
				65				70						75	
Ser	Arg	Tyr	Arg	Gly	Gln	Glu	His	Cys	Leu	His	Pro	Lys	Leu	Gln	
				80				85						90	
Ser	Thr	Lys	Arg	Phe	Ile	Lys	Trp	Tyr	Asn	Ala	Trp	Asn	Glu	Lys	
				95				100						105	
Arg	Arg	Val	Tyr	Glu	Glu										
				110											

<210> 371

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 371

cagcgccctc cccatgtccc tg 22

<210> 372

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 372

tcccaactgg tttggagttt tccc 24

<210> 373

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 373

ctccggtcag catgaggctc ctggcggccg ctgctcctgc tgctg 45

<210> 374

<211> 3113

<212> DNA

<213> Homo sapiens

<400> 374

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accctcattg acagccaagc acagtatcca gttgtcaaca caaattatgg 150

caaaatccgg ggcctaagaa caccgttacc caatgagatc ttgggtccag 200

tggagcagta cttaggggtc ccctatgcct cccccccac tggagagagg 250

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tgcatgacat gctgcccac tggtttaccg ccaatttgga tactttgatg 400

acctatgttc aagatcaaaa tgaagactgc ctttacttaa acatctacgt 450

gcccacggaa gatggagcca acacaaagaa aaacgcagat gatataacga 500

gtaatgaccg tggatgaagac gaagatattc atgatcagaa cagtaagaag 550

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ccattaacta ccgtctggga atactagggt ttttaagtac cggtgaccag 700

gcagcaaaaag gcaactatgg gtcctggat cagattcaag cactgcggtg 750

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tctttggctc gggggctggg gcctcctgtg tcagcctgtt gaccctgtcc 850

cactactcag aaggtctctt ccagaaggcc atcattcaga gcggcaccgc 900

cctgtccagc tgggcagtga actaccagcc ggccaagtac actcggatat 950

tggcagacaa ggtcggctgc aacatgctgg acaccacgga catggtagaa 1000

tgcttgcgga acaagaacta caaggagctc atccagcaga ccatcacccc 1050

ggccacctac cacatagcct tcgggccggt gatcgacggc gacgtcatcc 1100

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<210> 375

<211> 816

<212> PRT

<213> Homo sapiens

<400> 375

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Lys	Phe	Thr	Leu	Ile	Asp	Ser	Gln	Ala	Gln	Tyr	Pro	Val	Val	Asn
				20					25					30
Thr	Asn	Tyr	Gly	Lys	Ile	Arg	Gly	Leu	Arg	Thr	Pro	Leu	Pro	Asn
				35					40					45
Glu	Ile	Leu	Gly	Pro	Val	Glu	Gln	Tyr	Leu	Gly	Val	Pro	Tyr	Ala
				50					55					60
Ser	Pro	Pro	Thr	Gly	Glu	Arg	Arg	Phe	Gln	Pro	Pro	Glu	Pro	Pro
				65					70					75
Ser	Ser	Trp	Thr	Gly	Ile	Arg	Asn	Thr	Thr	Gln	Phe	Ala	Ala	Val
				80					85					90
Cys	Pro	Gln	His	Leu	Asp	Glu	Arg	Ser	Leu	Leu	His	Asp	Met	Leu
				95					100					105
Pro	Ile	Trp	Phe	Thr	Ala	Asn	Leu	Asp	Thr	Leu	Met	Thr	Tyr	Val
				110					115					120
Gln	Asp	Gln	Asn	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Ile	Tyr	Val	Pro
				125					130					135
Thr	Glu	Asp	Gly	Ala	Asn	Thr	Lys	Lys	Asn	Ala	Asp	Asp	Ile	Thr
				140					145					150

Ser	Asn	Asp	Arg	Gly	Glu	Asp	Glu	Asp	Ile	His	Asp	Gln	Asn	Ser	
				155					160					165	
Lys	Lys	Pro	Val	Met	Val	Tyr	Ile	His	Gly	Gly	Ser	Tyr	Met	Glu	
				170					175					180	
Gly	Thr	Gly	Asn	Met	Ile	Asp	Gly	Ser	Ile	Leu	Ala	Ser	Tyr	Gly	
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Asn	Val	Ile	Val	Ile	Thr	Ile	Asn	Tyr	Arg	Leu	Gly	Ile	Leu	Gly	
				200					205					210	
Phe	Leu	Ser	Thr	Gly	Asp	Gln	Ala	Ala	Lys	Gly	Asn	Tyr	Gly	Leu	
				215					220					225	
Leu	Asp	Gln	Ile	Gln	Ala	Leu	Arg	Trp	Ile	Glu	Glu	Asn	Val	Gly	
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Ala	Phe	Gly	Gly	Asp	Pro	Lys	Arg	Val	Thr	Ile	Phe	Gly	Ser	Gly	
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Ala	Gly	Ala	Ser	Cys	Val	Ser	Leu	Leu	Thr	Leu	Ser	His	Tyr	Ser	
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Glu	Gly	Leu	Phe	Gln	Lys	Ala	Ile	Ile	Gln	Ser	Gly	Thr	Ala	Leu	
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Ser	Ser	Trp	Ala	Val	Asn	Tyr	Gln	Pro	Ala	Lys	Tyr	Thr	Arg	Ile	
				290					295					300	
Leu	Ala	Asp	Lys	Val	Gly	Cys	Asn	Met	Leu	Asp	Thr	Thr	Asp	Met	
				305					310					315	
Val	Glu	Cys	Leu	Arg	Asn	Lys	Asn	Tyr	Lys	Glu	Leu	Ile	Gln	Gln	
				320					325					330	
Thr	Ile	Thr	Pro	Ala	Thr	Tyr	His	Ile	Ala	Phe	Gly	Pro	Val	Ile	
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Asp	Gly	Asp	Val	Ile	Pro	Asp	Asp	Pro	Gln	Ile	Leu	Met	Glu	Gln	
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Gly	Glu	Phe	Leu	Asn	Tyr	Asp	Ile	Met	Leu	Gly	Val	Asn	Gln	Gly	
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Glu	Gly	Leu	Lys	Phe	Val	Asp	Gly	Ile	Val	Asp	Asn	Glu	Asp	Gly	
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Val	Thr	Pro	Asn	Asp	Phe	Asp	Phe	Ser	Val	Ser	Asn	Phe	Val	Asp	
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Asn	Leu	Tyr	Gly	Tyr	Pro	Glu	Gly	Lys	Asp	Thr	Leu	Arg	Glu	Thr	
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Ile	Lys	Phe	Met	Tyr	Thr	Asp	Trp	Ala	Asp	Lys	Glu	Asn	Pro	Glu	
				425					430					435	

Thr Arg Arg Lys	Thr Leu Val Ala Leu	Phe Thr Asp His Gln	Trp
440		445	450
Val Ala Pro Ala	Val Ala Ala Asp Leu	His Ala Gln Tyr Gly	Ser
455		460	465
Pro Thr Tyr Phe	Tyr Ala Phe Tyr His	His Cys Gln Ser Glu	Met
470		475	480
Lys Pro Ser Trp	Ala Asp Ser Ala His	Gly Asp Glu Val Pro	Tyr
485		490	495
Val Phe Gly Ile	Pro Met Ile Gly Pro	Thr Glu Leu Phe Ser	Cys
500		505	510
Asn Phe Ser Lys	Asn Asp Val Met Leu	Ser Ala Val Val Met	Thr
515		520	525
Tyr Trp Thr Asn	Phe Ala Lys Thr Gly	Asp Pro Asn Gln Pro	Val
530		535	540
Pro Gln Asp Thr	Lys Phe Ile His Thr	Lys Pro Asn Arg Phe	Glu
545		550	555
Glu Val Ala Trp	Ser Lys Tyr Asn Pro	Lys Asp Gln Leu Tyr	Leu
560		565	570
His Ile Gly Leu	Lys Pro Arg Val Arg	Asp His Tyr Arg Ala	Thr
575		580	585
Lys Val Ala Phe	Trp Leu Glu Leu Val	Pro His Leu His Asn	Leu
590		595	600
Asn Glu Ile Phe	Gln Tyr Val Ser Thr	Thr Thr Lys Val Pro	Pro
605		610	615
Pro Asp Met Thr	Ser Phe Pro Tyr Gly	Thr Arg Arg Ser Pro	Ala
620		625	630
Lys Ile Trp Pro	Thr Thr Lys Arg Pro	Ala Ile Thr Pro Ala	Asn
635		640	645
Asn Pro Lys His	Ser Lys Asp Pro His	Lys Thr Gly Pro Glu	Asp
650		655	660
Thr Thr Val Leu	Ile Glu Thr Lys Arg	Asp Tyr Ser Thr Glu	Leu
665		670	675
Ser Val Thr Ile	Ala Val Gly Ala Ser	Leu Leu Phe Leu Asn	Ile
680		685	690
Leu Ala Phe Ala	Ala Leu Tyr Tyr Lys	Lys Asp Lys Arg Arg	His
695		700	705
Glu Thr His Arg	Arg Pro Ser Pro Gln	Arg Asn Thr Thr Asn	Asp
710		715	720

Ile	Ala	His	Ile	Gln	Asn	Glu	Glu	Ile	Met	Ser	Leu	Gln	Met	Lys
				725					730					735
Gln	Leu	Glu	His	Asp	His	Glu	Cys	Glu	Ser	Leu	Gln	Ala	His	Asp
				740					745					750
Thr	Leu	Arg	Leu	Thr	Cys	Pro	Pro	Asp	Tyr	Thr	Leu	Thr	Leu	Arg
				755					760					765
Arg	Ser	Pro	Asp	Asp	Ile	Pro	Leu	Met	Thr	Pro	Asn	Thr	Ile	Thr
				770					775					780
Met	Ile	Pro	Asn	Thr	Leu	Thr	Gly	Met	Gln	Pro	Leu	His	Thr	Phe
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Asn	Thr	Phe	Ser	Gly	Gly	Gln	Asn	Ser	Thr	Asn	Leu	Pro	His	Gly
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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 376

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<210> 377

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 377

aacccccgag ccaaaagatg gtcac 25

<210> 378

<211> 47

<212> DNA

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<223> Synthetic oligonucleotide probe

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<210> 379

<211> 2461

<212> DNA

<213> Homo sapiens

<400> 379

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<210> 380

<211> 348

<212> PRT

<213> Homo sapiens

<400> 380

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				20				25					30	

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Gln	Thr	Phe	Glu	Tyr 50	Leu	Lys	Arg	Glu	His 55	Ser	Leu	Ser	Lys	Pro 60
Tyr	Gln	Gly	Val	Gly 65	Thr	Gly	Ser	Ser	Ser 70	Leu	Trp	Asn	Leu	Met 75
Gly	Asn	Ala	Met	Val 80	Met	Thr	Gln	Tyr	Ile 85	Arg	Leu	Thr	Pro	Asp 90
Met	Gln	Ser	Lys	Gln 95	Gly	Ala	Leu	Trp	Asn 100	Arg	Val	Pro	Cys	Phe 105
Leu	Arg	Asp	Trp	Glu 110	Leu	Gln	Val	His	Phe 115	Lys	Ile	His	Gly	Gln 120
Gly	Lys	Lys	Asn	Leu 125	His	Gly	Asp	Gly	Leu 130	Ala	Ile	Trp	Tyr	Thr 135
Lys	Asp	Arg	Met	Gln 140	Pro	Gly	Pro	Val	Phe 145	Gly	Asn	Met	Asp	Lys 150
Phe	Val	Gly	Leu	Gly 155	Val	Phe	Val	Asp	Thr 160	Tyr	Pro	Asn	Glu	Glu 165
Lys	Gln	Gln	Glu	Arg 170	Val	Phe	Pro	Tyr	Ile 175	Ser	Ala	Met	Val	Asn 180
Asn	Gly	Ser	Leu	Ser 185	Tyr	Asp	His	Glu	Arg 190	Asp	Gly	Arg	Pro	Thr 195
Glu	Leu	Gly	Gly	Cys 200	Thr	Ala	Ile	Val	Arg 205	Asn	Leu	His	Tyr	Asp 210
Thr	Phe	Leu	Val	Ile 215	Arg	Tyr	Val	Lys	Arg 220	His	Leu	Thr	Ile	Met 225
Met	Asp	Ile	Asp	Gly 230	Lys	His	Glu	Trp	Arg 235	Asp	Cys	Ile	Glu	Val 240
Pro	Gly	Val	Arg	Leu 245	Pro	Arg	Gly	Tyr	Tyr 250	Phe	Gly	Thr	Ser	Ser 255
Ile	Thr	Gly	Asp	Leu 260	Ser	Asp	Asn	His	Asp 265	Val	Ile	Ser	Leu	Lys 270
Leu	Phe	Glu	Leu	Thr 275	Val	Glu	Arg	Thr	Pro 280	Glu	Glu	Glu	Lys	Leu 285
His	Arg	Asp	Val	Phe 290	Leu	Pro	Ser	Val	Asp 295	Asn	Met	Lys	Leu	Pro 300
Glu	Met	Thr	Ala	Pro 305	Leu	Pro	Pro	Leu	Ser 310	Gly	Leu	Ala	Leu	Phe 315

Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val
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Arg Phe Tyr

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<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 381

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<210> 382

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 383

<211> 45

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 383

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<210> 384

<211> 3150

<212> DNA

<213> Homo sapiens

<400> 384

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gtgttgcatt tgaatatgtc tgtttctata aataaatttt ttaagaataa 3150

<210> 385

<211> 480

<212> PRT

<213> Homo sapiens

<400> 385

Met Leu Phe Arg Asn Arg Phe Leu Leu Leu Leu Ala Leu Ala Ala
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Leu Leu Ala Phe Val Ser Leu Ser Leu Gln Phe Phe His Leu Ile
20 25 30

Pro Val Ser Thr Pro Lys Asn Gly Met Ser Ser Lys Ser Arg Lys
35 40 45

Arg Ile Met Pro Asp Pro Val Thr Glu Pro Pro Val Thr Asp Pro
50 55 60

Val Tyr Glu Ala Leu Leu Tyr Cys Asn Ile Pro Ser Val Ala Glu
65 70 75

Arg Ser Met Glu Gly His Ala Pro His His Phe Lys Leu Val Ser
80 85 90

Val His Val Phe Ile Arg His Gly Asp Arg Tyr Pro Leu Tyr Val
95 100 105

Ile Pro Lys Thr Lys Arg Pro Glu Ile Asp Cys Thr Leu Val Ala
110 115 120

Asn Arg Lys Pro Tyr His Pro Lys Leu Glu Ala Phe Ile Ser His
125 130 135

Met Ser Lys Gly Ser Gly Ala Ser Phe Glu Ser Pro Leu Asn Ser
140 145 150

Leu Pro Leu Tyr Pro Asn His Pro Leu Cys Glu Met Gly Glu Leu
155 160 165

Thr Gln Thr Gly Val Val Gln His Leu Gln Asn Gly Gln Leu Leu
170 175 180

Arg Asp Ile Tyr Leu Lys Lys His Lys Leu Leu Pro Asn Asp Trp
185 190 195

Ser Ala Asp Gln Leu Tyr Leu Glu Thr Thr Gly Lys Ser Arg Thr
200 205 210

Leu Gln Ser Gly Leu Ala Leu Leu Tyr Gly Phe Leu Pro Asp Phe
215 220 225

Asp Trp Lys Lys Ile Tyr Phe Arg His Gln Pro Ser Ala Leu Phe
230 235 240

Cys Ser Gly Ser Cys Tyr Cys Pro Val Arg Asn Gln Tyr Leu Glu	245	250	255
Lys Glu Gln Arg Arg Gln Tyr Leu Leu Arg Leu Lys Asn Ser Gln	260	265	270
Leu Glu Lys Thr Tyr Gly Glu Met Ala Lys Ile Val Asp Val Pro	275	280	285
Thr Lys Gln Leu Arg Ala Ala Asn Pro Ile Asp Ser Met Leu Cys	290	295	300
His Phe Cys His Asn Val Ser Phe Pro Cys Thr Arg Asn Gly Cys	305	310	315
Val Asp Met Glu His Phe Lys Val Ile Lys Thr His Gln Ile Glu	320	325	330
Asp Glu Arg Glu Arg Arg Glu Lys Lys Leu Tyr Phe Gly Tyr Ser	335	340	345
Leu Leu Gly Ala His Pro Ile Leu Asn Gln Thr Ile Gly Arg Met	350	355	360
Gln Arg Ala Thr Glu Gly Arg Lys Glu Glu Leu Phe Ala Leu Tyr	365	370	375
Ser Ala His Asp Val Thr Leu Ser Pro Val Leu Ser Ala Leu Gly	380	385	390
Leu Ser Glu Ala Arg Phe Pro Arg Phe Ala Ala Arg Leu Ile Phe	395	400	405
Glu Leu Trp Gln Asp Arg Glu Lys Pro Ser Glu His Ser Val Arg	410	415	420
Ile Leu Tyr Asn Gly Val Asp Val Thr Phe His Thr Ser Phe Cys	425	430	435
Gln Asp His His Lys Arg Ser Pro Lys Pro Met Cys Pro Leu Glu	440	445	450
Asn Leu Val Arg Phe Val Lys Arg Asp Met Phe Val Ala Leu Gly	455	460	465
Gly Ser Gly Thr Asn Tyr Tyr Asp Ala Cys His Arg Glu Gly Phe	470	475	480

<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 386
 ccaagcagct tagagctcca gacc 24

<210> 387
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 387
 ttccctatgc tctgtattgg catgg 25

<210> 388
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 388
 gccacttctg ccacaatgtc agctttccct gtaccagaaa tggctgtgtt 50

<210> 389
 <211> 3313
 <212> DNA
 <213> Homo sapiens

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 aaaaaagctc actaaagttt ctattagagc gaatacggta gatttccatc 50
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 gccgctgttc accaatcggg gagagaaaag cggagatcct gctcgccttg 200
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aaactctatc tca 3313

<210> 390

<211> 916

<212> PRT

<213> Homo sapiens

<400> 390

Met	Ile	Pro	Ala	Arg	Leu	His	Arg	Asp	Tyr	Lys	Gly	Leu	Val	Leu		1	5	10	15
Leu	Gly	Ile	Leu	Leu	Gly	Thr	Leu	Trp	Glu	Thr	Gly	Cys	Thr	Gln		20	25	30	
Ile	Arg	Tyr	Ser	Val	Pro	Glu	Glu	Leu	Glu	Lys	Gly	Ser	Arg	Val		35	40	45	
Gly	Asp	Ile	Ser	Arg	Asp	Leu	Gly	Leu	Glu	Pro	Arg	Glu	Leu	Ala		50	55	60	
Glu	Arg	Gly	Val	Arg	Ile	Ile	Pro	Arg	Gly	Arg	Thr	Gln	Leu	Phe		65	70	75	
Ala	Leu	Asn	Pro	Arg	Ser	Gly	Ser	Leu	Val	Thr	Ala	Gly	Arg	Ile		80	85	90	
Asp	Arg	Glu	Glu	Leu	Cys	Met	Gly	Ala	Ile	Lys	Cys	Gln	Leu	Asn		95	100	105	
Leu	Asp	Ile	Leu	Met	Glu	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Val	Glu		110	115	120	
Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Tyr	Phe	Arg	Glu		125	130	135	
Ser	Glu	Leu	Glu	Ile	Lys	Ile	Ser	Glu	Asn	Ala	Ala	Thr	Glu	Met		140	145	150	
Arg	Phe	Pro	Leu	Pro	His	Ala	Trp	Asp	Pro	Asp	Ile	Gly	Lys	Asn		155	160	165	
Ser	Leu	Gln	Ser	Tyr	Glu	Leu	Ser	Pro	Asn	Thr	His	Phe	Ser	Leu		170	175	180	
Ile	Val	Gln	Asn	Gly	Ala	Asp	Gly	Ser	Lys	Tyr	Pro	Glu	Leu	Val		185	190	195	
Leu	Lys	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Lys	Ala	Ala	His	His	Leu		200	205	210	
Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Asp	Pro	Val	Arg	Thr	Gly	Thr		215	220	225	
Ala	Arg	Ile	Arg	Val	Met	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro		230	235	240	
Ala	Phe	Ala	Gln	Pro	Glu	Tyr	Arg	Ala	Ser	Val	Pro	Glu	Asn	Leu		245	250	255	
Ala	Leu	Gly	Thr	Gln	Leu	Leu	Val	Val	Asn	Ala	Thr	Asp	Pro	Asp		260	265	270	
Glu	Gly	Val	Asn	Ala	Glu	Val	Arg	Tyr	Ser	Phe	Arg	Tyr	Val	Asp		275	280	285	

Asp Lys Ala Ala Gln Val Phe Lys Leu Asp Cys Asn Ser Gly Thr	290	295	300
Ile Ser Thr Ile Gly Glu Leu Asp His Glu Glu Ser Gly Phe Tyr	305	310	315
Gln Met Glu Val Gln Ala Met Asp Asn Ala Gly Tyr Ser Ala Arg	320	325	330
Ala Lys Val Leu Ile Thr Val Leu Asp Val Asn Asp Asn Ala Pro	335	340	345
Glu Val Val Leu Thr Ser Leu Ala Ser Ser Val Pro Glu Asn Ser	350	355	360
Pro Arg Gly Thr Leu Ile Ala Leu Leu Asn Val Asn Asp Gln Asp	365	370	375
Ser Glu Glu Asn Gly Gln Val Ile Cys Phe Ile Gln Gly Asn Leu	380	385	390
Pro Phe Lys Leu Glu Lys Ser Tyr Gly Asn Tyr Tyr Ser Leu Val	395	400	405
Thr Asp Ile Val Leu Asp Arg Glu Gln Val Pro Ser Tyr Asn Ile	410	415	420
Thr Val Thr Ala Thr Asp Arg Gly Thr Pro Pro Leu Ser Thr Glu	425	430	435
Thr His Ile Ser Leu Asn Val Ala Asp Thr Asn Asp Asn Pro Pro	440	445	450
Val Phe Pro Gln Ala Ser Tyr Ser Ala Tyr Ile Pro Glu Asn Asn	455	460	465
Pro Arg Gly Val Ser Leu Val Ser Val Thr Ala His Asp Pro Asp	470	475	480
Cys Glu Glu Asn Ala Gln Ile Thr Tyr Ser Leu Ala Glu Asn Thr	485	490	495
Ile Gln Gly Ala Ser Leu Ser Ser Tyr Val Ser Ile Asn Ser Asp	500	505	510
Thr Gly Val Leu Tyr Ala Leu Ser Ser Phe Asp Tyr Glu Gln Phe	515	520	525
Arg Asp Leu Gln Val Lys Val Met Ala Arg Asp Asn Gly His Pro	530	535	540
Pro Leu Ser Ser Asn Val Ser Leu Ser Leu Phe Val Leu Asp Gln	545	550	555
Asn Asp Asn Ala Pro Glu Ile Leu Tyr Pro Ala Leu Pro Thr Asp	560	565	570

Gly Ser Thr Gly Val Glu Leu Ala Pro Arg Ser Ala Glu Pro Gly	575	580	585
Tyr Leu Val Thr Lys Val Val Ala Val Asp Arg Asp Ser Gly Gln	590	595	600
Asn Ala Trp Leu Ser Tyr Arg Leu Leu Lys Ala Ser Glu Pro Gly	605	610	615
Leu Phe Ser Val Gly Leu His Thr Gly Glu Val Arg Thr Ala Arg	620	625	630
Ala Leu Leu Asp Arg Asp Ala Leu Lys Gln Ser Leu Val Val Ala	635	640	645
Val Gln Asp His Gly Gln Pro Pro Leu Ser Ala Thr Val Thr Leu	650	655	660
Thr Val Ala Val Ala Asp Ser Ile Pro Gln Val Leu Ala Asp Leu	665	670	675
Gly Ser Leu Glu Ser Pro Ala Asn Ser Glu Thr Ser Asp Leu Thr	680	685	690
Leu Tyr Leu Val Val Ala Val Ala Ala Val Ser Cys Val Phe Leu	695	700	705
Ala Phe Val Ile Leu Leu Leu Ala Leu Arg Leu Arg Arg Trp His	710	715	720
Lys Ser Arg Leu Leu Gln Ala Ser Gly Gly Gly Leu Thr Gly Ala	725	730	735
Pro Ala Ser His Phe Val Gly Val Asp Gly Val Gln Ala Phe Leu	740	745	750
Gln Thr Tyr Ser His Glu Val Ser Leu Thr Thr Asp Ser Arg Lys	755	760	765
Ser His Leu Ile Phe Pro Gln Pro Asn Tyr Ala Asp Met Leu Val	770	775	780
Ser Gln Glu Ser Phe Glu Lys Ser Glu Pro Leu Leu Leu Ser Gly	785	790	795
Asp Ser Val Phe Ser Lys Asp Ser His Gly Leu Ile Glu Val Ser	800	805	810
Leu Tyr Gln Ile Phe Phe Leu Phe Phe Phe Asn Cys Ser Val Ser	815	820	825
Gln Ala Gly Val Gln Arg Tyr Asp His Ser Ser Leu Arg Pro Gln	830	835	840
Thr Pro Arg Leu Lys Gln Leu Ser His Leu Cys Leu Arg Cys Asn	845	850	855

Arg	Asp	Tyr	Arg	Cys	Lys	Pro	Pro	Thr	Val	Cys	Leu	Ser	Ile	Tyr
				860					865					870
Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Leu	Leu
				875					880					885
Ser	Cys	Thr	Asp	Gly	Ser	Leu	Thr	Pro	Val	Ile	Pro	Val	Leu	Trp
				890					895					900
Glu	Ala	Glu	Ala	Gly	Gly	Ser	Pro	Glu	Val	Gly	Ser	Leu	Arg	Pro
				905					910					915

Ala

<210> 391

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

tccgtctctg tgaaccgccc cac 23

<210> 392

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

ctcgggcgca ttgtcgttct ggtc 24

<210> 393

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

ccgactgtga aagagaacgc cccagatcca cttgttcccc 40

<210> 394

<211> 999

<212> DNA

<213> Homo sapiens

<400> 394

cccaggctct agtgcaggag gagaaggagg aggagcagga ggtggagatt 50

cccagttaaa aggctccaga atcgtgtacc aggagagaa ctgaagtact 100

ggggcctcct ccactgggtc cgaatcagta ggtgaceccg cccctggatt 150
 ctggaagacc tcaccatggg acgccccga cctcgtgcgg ccaagacgtg 200
 gatgttcctg ctcttgctgg ggggagcctg ggcaggacac tccagggcac 250
 aggaggacaa ggtgctgggg ggtcatgagt gccaacccca ttcgcagcct 300
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<210> 395

<211> 260

<212> PRT

<213> Homo sapiens

<400> 395

Met	Gly	Arg	Pro	Arg	Pro	Arg	Ala	Ala	Lys	Thr	Trp	Met	Phe	Leu
1				5					10					15

Leu	Leu	Leu	Gly	Gly	Ala	Trp	Ala	Gly	His	Ser	Arg	Ala	Gln	Glu
			20						25					30

Asp	Lys	Val	Leu	Gly	Gly	His	Glu	Cys	Gln	Pro	His	Ser	Gln	Pro
				35					40					45

Trp	Gln	Ala	Ala	Leu	Phe	Gln	Gly	Gln	Gln	Leu	Leu	Cys	Gly	Gly
				50					55					60

Val	Leu	Val	Gly	Gly	Asn	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Lys
				65					70					75

Lys	Pro	Lys	Tyr	Thr	Val	Arg	Leu	Gly	Asp	His	Ser	Leu	Gln	Asn	80	85	90
Lys	Asp	Gly	Pro	Glu	Gln	Glu	Ile	Pro	Val	Val	Gln	Ser	Ile	Pro	95	100	105
His	Pro	Cys	Tyr	Asn	Ser	Ser	Asp	Val	Glu	Asp	His	Asn	His	Asp	110	115	120
Leu	Met	Leu	Leu	Gln	Leu	Arg	Asp	Gln	Ala	Ser	Leu	Gly	Ser	Lys	125	130	135
Val	Lys	Pro	Ile	Ser	Leu	Ala	Asp	His	Cys	Thr	Gln	Pro	Gly	Gln	140	145	150
Lys	Cys	Thr	Val	Ser	Gly	Trp	Gly	Thr	Val	Thr	Ser	Pro	Arg	Glu	155	160	165
Asn	Phe	Pro	Asp	Thr	Leu	Asn	Cys	Ala	Glu	Val	Lys	Ile	Phe	Pro	170	175	180
Gln	Lys	Lys	Cys	Glu	Asp	Ala	Tyr	Pro	Gly	Gln	Ile	Thr	Asp	Gly	185	190	195
Met	Val	Cys	Ala	Gly	Ser	Ser	Lys	Gly	Ala	Asp	Thr	Cys	Gln	Gly	200	205	210
Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asp	Gly	Ala	Leu	Gln	Gly	Ile	215	220	225
Thr	Ser	Trp	Gly	Ser	Asp	Pro	Cys	Gly	Arg	Ser	Asp	Lys	Pro	Gly	230	235	240
Val	Tyr	Thr	Asn	Ile	Cys	Arg	Tyr	Leu	Asp	Trp	Ile	Lys	Lys	Ile	245	250	255
Ile	Gly	Ser	Lys	Gly											260		

<210> 396

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 396

cagcctacag aataaagatg gccc 24

<210> 397

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 397

ggtgcaatga tctgccaggc tgat 24

<210> 398

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

agaaatacct gtggttcagt ccaccccaaa cccctgctac aacagcag 48

<210> 399

<211> 2236

<212> DNA

<213> Homo sapiens

<400> 399

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gccccgccc gggcccgcgc ccgcgcccgc gccaggtga gcgctccgcc 150
cgccgcgagg ccccgccccg gcccgcccc gcccgcccc ggccggcggg 200
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 aatgactcac cctttgggac tctgcctggc tctgctgagc cccgctcac 1700
 tgcaagtgcg cccgagggct ccgagccacc agggttcccc acctcgggcc 1750
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 ccgccaagcc agccgggcg ccgacccgtg gggcaggcca ggccaggtcc 2050
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<210> 400

<211> 473

<212> PRT
<213> Homo sapiens

<400> 400

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Leu	Trp	Leu	Gln	Ala	Trp	Gln	Val	Ala	Ala	Pro	Cys	Pro	Gly	Ala	
			20						25					30	
Cys	Val	Cys	Tyr	Asn	Glu	Pro	Lys	Val	Thr	Thr	Ser	Cys	Pro	Gln	
			35						40					45	
Gln	Gly	Leu	Gln	Ala	Val	Pro	Val	Gly	Ile	Pro	Ala	Ala	Ser	Gln	
			50						55					60	
Arg	Ile	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	His	Val	Pro	Ala	Ala	
			65						70					75	
Ser	Phe	Arg	Ala	Cys	Arg	Asn	Leu	Thr	Ile	Leu	Trp	Leu	His	Ser	
			80						85					90	
Asn	Val	Leu	Ala	Arg	Ile	Asp	Ala	Ala	Ala	Phe	Thr	Gly	Leu	Ala	
			95						100					105	
Leu	Leu	Glu	Gln	Leu	Asp	Leu	Ser	Asp	Asn	Ala	Gln	Leu	Arg	Ser	
			110						115					120	
Val	Asp	Pro	Ala	Thr	Phe	His	Gly	Leu	Gly	Arg	Leu	His	Thr	Leu	
			125						130					135	
His	Leu	Asp	Arg	Cys	Gly	Leu	Gln	Glu	Leu	Gly	Pro	Gly	Leu	Phe	
			140						145					150	
Arg	Gly	Leu	Ala	Ala	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	Ala	
			155						160					165	
Leu	Gln	Ala	Leu	Pro	Asp	Asp	Thr	Phe	Arg	Asp	Leu	Gly	Asn	Leu	
			170						175					180	
Thr	His	Leu	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	Ser	Val	Pro	Glu	
			185						190					195	
Arg	Ala	Phe	Arg	Gly	Leu	His	Ser	Leu	Asp	Arg	Leu	Leu	Leu	His	
			200						205					210	
Gln	Asn	Arg	Val	Ala	His	Val	His	Pro	His	Ala	Phe	Arg	Asp	Leu	
			215						220					225	
Gly	Arg	Leu	Met	Thr	Leu	Tyr	Leu	Phe	Ala	Asn	Asn	Leu	Ser	Ala	
			230						235					240	
Leu	Pro	Thr	Glu	Ala	Leu	Ala	Pro	Leu	Arg	Ala	Leu	Gln	Tyr	Leu	
			245						250					255	
Arg	Leu	Asn	Asp	Asn	Pro	Trp	Val	Cys	Asp	Cys	Arg	Ala	Arg	Pro	
			260						265					270	

Leu Trp Ala Trp	Leu Gln Lys Phe Arg	Gly Ser Ser Ser	Glu Val
275		280	285
Pro Cys Ser Leu	Pro Gln Arg Leu Ala	Gly Arg Asp Leu Lys	Arg
290		295	300
Leu Ala Ala Asn	Asp Leu Gln Gly Cys	Ala Val Ala Thr	Gly Pro
305		310	315
Tyr His Pro Ile	Trp Thr Gly Arg Ala	Thr Asp Glu Glu	Pro Leu
320		325	330
Gly Leu Pro Lys	Cys Cys Gln Pro Asp	Ala Ala Asp Lys	Ala Ser
335		340	345
Val Leu Glu Pro	Gly Arg Pro Ala Ser	Ala Gly Asn Ala	Leu Lys
350		355	360
Gly Arg Val Pro	Pro Gly Asp Ser Pro	Pro Gly Asn Gly	Ser Gly
365		370	375
Pro Arg His Ile	Asn Asp Ser Pro Phe	Gly Thr Leu Pro	Gly Ser
380		385	390
Ala Glu Pro Pro	Leu Thr Ala Val Arg	Pro Glu Gly Ser	Glu Pro
395		400	405
Pro Gly Phe Pro	Thr Ser Gly Pro Arg	Arg Arg Pro Gly	Cys Ser
410		415	420
Arg Lys Asn Arg	Thr Arg Ser His Cys	Arg Leu Gly Gln	Ala Gly
425		430	435
Ser Gly Gly Gly	Gly Thr Gly Asp Ser	Glu Gly Ser Gly	Ala Leu
440		445	450
Pro Ser Leu Thr	Cys Ser Leu Thr Pro	Leu Gly Leu Ala	Leu Val
455		460	465
Leu Trp Thr Val	Leu Gly Pro Cys		
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<210> 401

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 401

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<210> 402

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 403

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

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<210> 404

<211> 2738

<212> DNA

<213> Homo sapiens

<400> 404

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agctgaatcc agcaagaaca atggaggcca gcggggaagct catttgaga 200
caaaggcaag tccttttttc ctttctcctt ttgggcttat ctctggcggg 250
cgcgggcgga cctagaagct attctgtggt ggaggaaact gagggcagct 300
cctttgtcac caatttagca aaggacctgg gtctggagca gagggaattc 350
tccaggcggg gggttagggt tgtttccaga gggaacaaac tacatttgca 400
gctcaatcag gagaccgcgg atttgttgct aaatgagaaa ttggaccgtg 450
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ctagagagtc ctttcgagtt ttttcaagct gagctgcaag taatagacat 550
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<210> 405
 <211> 798
 <212> PRT
 <213> Homo sapiens

<400> 405
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 Phe Ser Phe Leu Leu Leu Gly Leu Ser Leu Ala Gly Ala Ala Glu
 20 25 30
 Pro Arg Ser Tyr Ser Val Val Glu Glu Thr Glu Gly Ser Ser Phe
 35 40 45
 Val Thr Asn Leu Ala Lys Asp Leu Gly Leu Glu Gln Arg Glu Phe
 50 55 60
 Ser Arg Arg Gly Val Arg Val Val Ser Arg Gly Asn Lys Leu His
 65 70 75
 Leu Gln Leu Asn Gln Glu Thr Ala Asp Leu Leu Leu Asn Glu Lys
 80 85 90
 Leu Asp Arg Glu Asp Leu Cys Gly His Thr Glu Pro Cys Val Leu
 95 100 105
 Arg Phe Gln Val Leu Leu Glu Ser Pro Phe Glu Phe Phe Gln Ala
 110 115 120
 Glu Leu Gln Val Ile Asp Ile Asn Asp His Ser Pro Val Phe Leu
 125 130 135
 Asp Lys Gln Met Leu Val Lys Val Ser Glu Ser Ser Pro Pro Gly
 140 145 150

Thr Thr Phe Pro	Leu Lys Asn Ala Glu Asp Leu Asp Val Gly Gln	155	160	165
Asn Asn Ile Glu	Asn Tyr Ile Ile Ser Pro Asn Ser Tyr Phe Arg	170	175	180
Val Leu Thr Arg	Lys Arg Ser Asp Gly Arg Lys Tyr Pro Glu Leu	185	190	195
Val Leu Asp Lys	Ala Leu Asp Arg Glu Glu Glu Ala Glu Leu Arg	200	205	210
Leu Thr Leu Thr	Ala Leu Asp Gly Gly Ser Pro Pro Arg Ser Gly	215	220	225
Thr Ala Gln Val	Tyr Ile Glu Val Leu Asp Val Asn Asp Asn Ala	230	235	240
Pro Glu Phe Glu	Gln Pro Phe Tyr Arg Val Gln Ile Ser Glu Asp	245	250	255
Ser Pro Val Gly	Phe Leu Val Val Lys Val Ser Ala Thr Asp Val	260	265	270
Asp Thr Gly Val	Asn Gly Glu Ile Ser Tyr Ser Leu Phe Gln Ala	275	280	285
Ser Glu Glu Ile	Gly Lys Thr Phe Lys Ile Asn Pro Leu Thr Gly	290	295	300
Glu Ile Glu Leu	Lys Lys Gln Leu Asp Phe Glu Lys Leu Gln Ser	305	310	315
Tyr Glu Val Asn	Ile Glu Ala Arg Asp Ala Gly Thr Phe Ser Gly	320	325	330
Lys Cys Thr Val	Leu Ile Gln Val Ile Asp Val Asn Asp His Ala	335	340	345
Pro Glu Val Thr	Met Ser Ala Phe Thr Ser Pro Ile Pro Glu Asn	350	355	360
Ala Pro Glu Thr	Val Val Ala Leu Phe Ser Val Ser Asp Leu Asp	365	370	375
Ser Gly Glu Asn	Gly Lys Ile Ser Cys Ser Ile Gln Glu Asp Leu	380	385	390
Pro Phe Leu Leu	Lys Ser Ala Glu Asn Phe Tyr Thr Leu Leu Thr	395	400	405
Glu Arg Pro Leu	Asp Arg Glu Ser Arg Ala Glu Tyr Asn Ile Thr	410	415	420
Ile Thr Val Thr	Asp Leu Gly Thr Pro Met Leu Ile Thr Gln Leu	425	430	435

Asn Met Thr Val	Leu Ile Ala Asp Val	Asn Asp Asn Ala Pro	Ala
440	445	450	
Phe Thr Gln Thr	Ser Tyr Thr Leu Phe	Val Arg Glu Asn Asn	Ser
455	460	465	
Pro Ala Leu His	Ile Arg Ser Val Ser	Ala Thr Asp Arg Asp	Ser
470	475	480	
Gly Thr Asn Ala	Gln Val Thr Tyr Ser	Leu Leu Pro Pro Gln	Asp
485	490	495	
Pro His Leu Pro	Leu Thr Ser Leu Val	Ser Ile Asn Ala Asp	Asn
500	505	510	
Gly His Leu Phe	Ala Leu Arg Ser Leu	Asp Tyr Glu Ala Leu	Gln
515	520	525	
Gly Phe Gln Phe	Arg Val Gly Ala Ser	Asp His Gly Ser Pro	Ala
530	535	540	
Leu Ser Ser Glu	Ala Leu Val Arg Val	Val Val Leu Asp Ala	Asn
545	550	555	
Asp Asn Ser Pro	Phe Val Leu Tyr Pro	Leu Gln Asn Gly Ser	Ala
560	565	570	
Pro Cys Thr Glu	Leu Val Pro Arg Ala	Ala Glu Pro Gly Tyr	Leu
575	580	585	
Val Thr Lys Val	Val Ala Val Asp Gly	Asp Ser Gly Gln Asn	Ala
590	595	600	
Trp Leu Ser Tyr	Gln Leu Leu Lys Ala	Thr Glu Leu Gly Leu	Phe
605	610	615	
Gly Val Trp Ala	His Asn Gly Glu Val	Arg Thr Ala Arg Leu	Leu
620	625	630	
Ser Glu Arg Asp	Ala Ala Lys His Arg	Leu Val Val Leu Val	Lys
635	640	645	
Asp Asn Gly Glu	Pro Pro Arg Ser Ala	Thr Ala Thr Leu His	Val
650	655	660	
Leu Leu Val Asp	Gly Phe Ser Gln Pro	Tyr Leu Pro Leu Pro	Glu
665	670	675	
Ala Ala Pro Thr	Gln Ala Gln Ala Asp	Leu Leu Thr Val Tyr	Leu
680	685	690	
Val Val Ala Leu	Ala Ser Val Ser Ser	Leu Phe Leu Phe Ser	Val
695	700	705	
Leu Leu Phe Val	Ala Val Arg Leu Cys	Arg Arg Ser Arg Ala	Ala
710	715	720	

Ser Val Gly Arg Cys Leu Val Pro Glu Gly Pro Leu Pro Gly His
725 730 735

Leu Val Asp Met Ser Gly Thr Arg Thr Leu Ser Gln Ser Tyr Gln
740 745 750

Tyr Glu Val Cys Leu Ala Gly Gly Ser Gly Thr Asn Glu Phe Lys
755 760 765

Phe Leu Lys Pro Ile Ile Pro Asn Phe Pro Pro Gln Cys Pro Gly
770 775 780

Lys Glu Ile Gln Gly Asn Ser Thr Phe Pro Asn Asn Phe Gly Phe
785 790 795

Asn Ile Gln

<210> 406

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 406

ctgagaacgc gcctgaaact gtg 23

<210> 407

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 407

agcgttgatca ttgacatcgg cg 22

<210> 408

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 408

ttagttgctc cattcaggag gatctaccct tcctcctgaa atccgcggaa 50

<210> 409

<211> 1379

<212> DNA

<213> Homo sapiens

<400> 409

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gcgtagccgt gcgccgattg cctctcggcc tgggcaatgg tcccggctgc 100
cggtcgacga ccgccccgcg tcatgcggct cctcggtggg tggcaagtat 150
tgctgtgggt gctgggactt cccgtccgcg gcgtggaggt tgcagaggaa 200
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acagggcagc agaagaggcc aatgcggtgc tggggctgga cacccaaggc 350
gatcacatgg tgatgctgtc tgtgattcct ggggaagctg aggacaaagt 400
gagttcagag cctagcggcg tcacctgtgg tgctggagga gcggaggact 450
caaggtgcaa cgtccgagag agccttttct ctctggatgg cgctggagca 500
cacttccttg acagagaaga ggagtattac acagagccag aagtggcgga 550
atctgacgca gccccgacag aggactccaa taacactgaa agtctgaaat 600
cccaaagggt gaactgtgag gagagaaaca ttacaggatt agaaaatttc 650
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gctcttcaact ttttggcact ggatgcatct cagcacagca gcctttctac 850
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aaccaatggc cagatttaat catacagatc gaacactgga aacactgaaa 950
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aactcaagcc gaccaaatag gccctcttcc cagcactttg ataaaaagt 1050
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<211> 360
<212> PRT
<213> Homo sapiens

<400> 410

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				20					25					30	
Arg	Gly	Val	Glu	Val	Ala	Glu	Glu	Ser	Gly	Arg	Leu	Trp	Ser	Glu	
				35					40					45	
Glu	Gln	Pro	Ala	His	Pro	Leu	Gln	Val	Gly	Ala	Val	Tyr	Leu	Gly	
				50					55					60	
Glu	Glu	Glu	Leu	Leu	His	Asp	Pro	Met	Gly	Gln	Asp	Arg	Ala	Ala	
				65					70					75	
Glu	Glu	Ala	Asn	Ala	Val	Leu	Gly	Leu	Asp	Thr	Gln	Gly	Asp	His	
				80					85					90	
Met	Val	Met	Leu	Ser	Val	Ile	Pro	Gly	Glu	Ala	Glu	Asp	Lys	Val	
				95					100					105	
Ser	Ser	Glu	Pro	Ser	Gly	Val	Thr	Cys	Gly	Ala	Gly	Gly	Ala	Glu	
				110					115					120	
Asp	Ser	Arg	Cys	Asn	Val	Arg	Glu	Ser	Leu	Phe	Ser	Leu	Asp	Gly	
				125					130					135	
Ala	Gly	Ala	His	Phe	Pro	Asp	Arg	Glu	Glu	Glu	Tyr	Tyr	Thr	Glu	
				140					145					150	
Pro	Glu	Val	Ala	Glu	Ser	Asp	Ala	Ala	Pro	Thr	Glu	Asp	Ser	Asn	
				155					160					165	
Asn	Thr	Glu	Ser	Leu	Lys	Ser	Pro	Lys	Val	Asn	Cys	Glu	Glu	Arg	
				170					175					180	
Asn	Ile	Thr	Gly	Leu	Glu	Asn	Phe	Thr	Leu	Lys	Ile	Leu	Asn	Met	
				185					190					195	
Ser	Gln	Asp	Leu	Met	Asp	Phe	Leu	Asn	Pro	Asn	Gly	Ser	Asp	Cys	
				200					205					210	
Thr	Leu	Val	Leu	Phe	Tyr	Thr	Pro	Trp	Cys	Arg	Phe	Ser	Ala	Ser	
				215					220					225	
Leu	Ala	Pro	His	Phe	Asn	Ser	Leu	Pro	Arg	Ala	Phe	Pro	Ala	Leu	
				230					235					240	
His	Phe	Leu	Ala	Leu	Asp	Ala	Ser	Gln	His	Ser	Ser	Leu	Ser	Thr	
				245					250					255	
Arg	Phe	Gly	Thr	Val	Ala	Val	Pro	Asn	Ile	Leu	Leu	Phe	Gln	Gly	

260	265	270
Ala Lys Pro Met	Ala Arg Phe Asn His Thr Asp Arg Thr Leu Glu	
275	280	285
Thr Leu Lys Ile	Phe Ile Phe Asn Gln Thr Gly Ile Glu Ala Lys	
290	295	300
Lys Asn Val Val	Val Thr Gln Ala Asp Gln Ile Gly Pro Leu Pro	
305	310	315
Ser Thr Leu Ile	Lys Ser Val Asp Trp Leu Leu Val Phe Ser Leu	
320	325	330
Phe Phe Leu Ile	Ser Phe Ile Met Tyr Ala Thr Ile Arg Thr Glu	
335	340	345
Ser Ile Arg Trp	Leu Ile Pro Gly Gln Glu Gln Glu His Val Glu	
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<210> 411

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 411

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<210> 412

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 412

ccacatgttc ctgctcttgt cctgg 25

<210> 413

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 413

cggtagtgac tgtactctag tcctgtttta caccctgtgg tgccg 45

<210> 414

<211> 1196

<212> DNA

<213> Homo sapiens

<400> 414

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<210> 415

<211> 295

<212> PRT

<213> Homo sapiens

<400> 415

Met Leu Gln Gly Pro Gly Ser Leu Leu Leu Leu Phe Leu Ala Ser

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His Cys Cys Leu Gly Ser Ala Arg Gly Leu Phe Leu Phe Gly Gln	20	25	30
Pro Asp Phe Ser Tyr Lys Arg Ser Asn Cys Lys Pro Ile Pro Val	35	40	45
Asn Leu Gln Leu Cys His Gly Ile Glu Tyr Gln Asn Met Arg Leu	50	55	60
Pro Asn Leu Leu Gly His Glu Thr Met Lys Glu Val Leu Glu Gln	65	70	75
Ala Gly Ala Trp Ile Pro Leu Val Met Lys Gln Cys His Pro Asp	80	85	90
Thr Lys Lys Phe Leu Cys Ser Leu Phe Ala Pro Val Cys Leu Asp	95	100	105
Asp Leu Asp Glu Thr Ile Gln Pro Cys His Ser Leu Cys Val Gln	110	115	120
Val Lys Asp Arg Cys Ala Pro Val Met Ser Ala Phe Gly Phe Pro	125	130	135
Trp Pro Asp Met Leu Glu Cys Asp Arg Phe Pro Gln Asp Asn Asp	140	145	150
Leu Cys Ile Pro Leu Ala Ser Ser Asp His Leu Leu Pro Ala Thr	155	160	165
Glu Glu Ala Pro Lys Val Cys Glu Ala Cys Lys Asn Lys Asn Asp	170	175	180
Asp Asp Asn Asp Ile Met Glu Thr Leu Cys Lys Asn Asp Phe Ala	185	190	195
Leu Lys Ile Lys Val Lys Glu Ile Thr Tyr Ile Asn Arg Asp Thr	200	205	210
Lys Ile Ile Leu Glu Thr Lys Ser Lys Thr Ile Tyr Lys Leu Asn	215	220	225
Gly Val Ser Glu Arg Asp Leu Lys Lys Ser Val Leu Trp Leu Lys	230	235	240
Asp Ser Leu Gln Cys Thr Cys Glu Glu Met Asn Asp Ile Asn Ala	245	250	255
Pro Tyr Leu Val Met Gly Gln Lys Gln Gly Gly Glu Leu Val Ile	260	265	270
Thr Ser Val Lys Arg Trp Gln Lys Gly Gln Arg Glu Phe Lys Arg	275	280	285
Ile Ser Arg Ser Ile Arg Lys Leu Gln Cys			

<210> 416

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 416

cctggctcgc tgctgctgct c 21

<210> 417

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 417

cctcacaggt gcaactgcaag ctgtc 25

<210> 418

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 418

ctcttctctt ttggccagcc cgacttctcc tacaagcgca gaattgc 47

<210> 419

<211> 1830

<212> DNA

<213> Homo sapiens

<400> 419

gtggaggccg ccgacgatgg cggggccgac ggaggccgag acgggggttg 50

ccgagccccg ggcctgtgac gcgcagcggg gccaccgcac ctacgcgcgc 100

cgctgggtgt tctgtctcgc gatcagcctg ctcaactgct ccaacgccac 150

gctgtggctc agctttgcac ctgtggctga cgtcattgct gaggacttgg 200

tctgtccat ggagcagatc aactggctgt cactgggtcta cctcgtggta 250

tccaccccat ttggcgtggc ggccatctgg atcctggact ccgtcgggct 300

ccgtgcggcg accatcctgg gtgcgtggct gaactttgcc gggagtgtgc 350

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gggagcgaat tacaagcgcg cacctgaaaa 1830

<210> 420
 <211> 560
 <212> PRT
 <213> Homo sapiens

<400> 420

Met	Ala	Gly	Pro	Thr	Glu	Ala	Glu	Thr	Gly	Leu	Ala	Glu	Pro	Arg	1	5	10	15
Ala	Leu	Cys	Ala	Gln	Arg	Gly	His	Arg	Thr	Tyr	Ala	Arg	Arg	Trp	20	25	30	
Val	Phe	Leu	Leu	Ala	Ile	Ser	Leu	Leu	Asn	Cys	Ser	Asn	Ala	Thr	35	40	45	
Leu	Trp	Leu	Ser	Phe	Ala	Pro	Val	Ala	Asp	Val	Ile	Ala	Glu	Asp	50	55	60	
Leu	Val	Leu	Ser	Met	Glu	Gln	Ile	Asn	Trp	Leu	Ser	Leu	Val	Tyr	65	70	75	
Leu	Val	Val	Ser	Thr	Pro	Phe	Gly	Val	Ala	Ala	Ile	Trp	Ile	Leu	80	85	90	
Asp	Ser	Val	Gly	Leu	Arg	Ala	Ala	Thr	Ile	Leu	Gly	Ala	Trp	Leu	95	100	105	
Asn	Phe	Ala	Gly	Ser	Val	Leu	Arg	Met	Val	Pro	Cys	Met	Val	Val	110	115	120	
Gly	Thr	Gln	Asn	Pro	Phe	Ala	Phe	Leu	Met	Gly	Gly	Gln	Ser	Leu	125	130	135	
Cys	Ala	Leu	Ala	Gln	Ser	Leu	Val	Ile	Phe	Ser	Pro	Ala	Lys	Leu	140	145	150	
Ala	Ala	Leu	Trp	Phe	Pro	Glu	His	Gln	Arg	Ala	Thr	Ala	Asn	Met	155	160	165	
Leu	Ala	Thr	Met	Ser	Asn	Pro	Leu	Gly	Val	Leu	Val	Ala	Asn	Val	170	175	180	
Leu	Ser	Pro	Val	Leu	Val	Lys	Lys	Gly	Glu	Asp	Ile	Pro	Leu	Met	185	190	195	
Leu	Gly	Val	Tyr	Thr	Ile	Pro	Ala	Gly	Val	Val	Cys	Leu	Leu	Ser	200	205	210	
Thr	Ile	Cys	Leu	Trp	Glu	Ser	Val	Pro	Pro	Thr	Pro	Pro	Ser	Ala	215	220	225	
Gly	Ala	Ala	Ser	Ser	Thr	Ser	Glu	Lys	Phe	Leu	Asp	Gly	Leu	Lys	230	235	240	
Leu	Gln	Leu	Met	Trp	Asn	Lys	Ala	Tyr	Val	Ile	Leu	Ala	Val	Cys	245	250	255	

Leu Gly Gly Met	Ile Gly Ile Ser Ala	Ser Phe Ser Ala Leu Leu	260	265	270
Glu Gln Ile Leu	Cys Ala Ser Gly His	Ser Ser Gly Phe Ser Gly	275	280	285
Leu Cys Gly Ala	Leu Phe Ile Thr Phe	Gly Ile Leu Gly Ala Leu	290	295	300
Ala Leu Gly Pro	Tyr Val Asp Arg Thr	Lys His Phe Thr Glu Ala	305	310	315
Thr Lys Ile Gly	Leu Cys Leu Phe Ser	Leu Ala Cys Val Pro Phe	320	325	330
Ala Leu Val Ser	Gln Leu Gln Gly Gln	Thr Leu Ala Leu Ala Ala	335	340	345
Thr Cys Ser Leu	Leu Gly Leu Phe Gly	Phe Ser Val Gly Pro Val	350	355	360
Ala Met Glu Leu	Ala Val Glu Cys Ser	Phe Pro Val Gly Glu Gly	365	370	375
Ala Ala Thr Gly	Met Ile Phe Val Leu	Gly Gln Ala Glu Gly Ile	380	385	390
Leu Ile Met Leu	Ala Met Thr Ala Leu	Thr Val Arg Arg Ser Glu	395	400	405
Pro Ser Leu Ser	Thr Cys Gln Gln Gly	Glu Asp Pro Leu Asp Trp	410	415	420
Thr Val Ser Leu	Leu Leu Met Ala Gly	Leu Cys Thr Phe Phe Ser	425	430	435
Cys Ile Leu Ala	Val Phe Phe His Thr	Pro Tyr Arg Arg Leu Gln	440	445	450
Ala Glu Ser Gly	Glu Pro Pro Ser Thr	Arg Asn Ala Val Gly Gly	455	460	465
Ala Asp Ser Gly	Pro Gly Val Asp Arg	Gly Gly Ala Gly Arg Ala	470	475	480
Gly Val Leu Gly	Pro Ser Thr Ala Thr	Pro Glu Cys Thr Ala Arg	485	490	495
Gly Ala Ser Leu	Glu Asp Pro Arg Gly	Pro Gly Ser Pro His Pro	500	505	510
Ala Cys His Arg	Ala Thr Pro Arg Ala	Gln Gly Pro Ala Ala Thr	515	520	525
Asp Ala Pro Ser	Arg Pro Gly Arg Leu	Ala Gly Arg Val Gln Ala	530	535	540

Ser Arg Phe Ile Asp Pro Ala Gly Ser His Ser Ser Phe Ser Ser
545 550 555

Pro Trp Val Ile Thr
560

<210> 421

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 421

agcttctcag ccctcctgga gcag 24

<210> 422

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 422

cggttcaata aacctggacg cttgg 25

<210> 423

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 423

tatgtggacc ggaccaagca cttcactgag gccaccaaga ttg 43

<210> 424

<211> 4313

<212> DNA

<213> Homo sapiens

<400> 424

gtccacatc ctgctcaact gggtcaggtc cctcttagac cagctcttgt 50

ccatcatttg ctgaagtgga ccaactagtt cccagtagg gggctctccc 100

tggaattct tgatcggcgt ttggacatct cagatcgctt ccaatgaaga 150

tggccttgcc ttggggctct gcttgtttca taatcatcta actatgggac 200

aaggttgtgc cggcagctct gggggaagga gcacggggct gatcaagcca 250

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<210> 425

<211> 1184

<212> PRT

<213> Homo sapiens

<400> 425

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1				5					10				15	

Gly Tyr Leu Phe Leu Leu Gly Asp Cys Gln Glu Val Thr Thr Leu	20	25	30
Thr Val Lys Tyr Gln Val Ser Glu Glu Val Pro Ser Gly Thr Val	35	40	45
Ile Gly Lys Leu Ser Gln Glu Leu Gly Arg Glu Glu Arg Arg Arg	50	55	60
Gln Ala Gly Ala Ala Phe Gln Val Leu Gln Leu Pro Gln Ala Leu	65	70	75
Pro Ile Gln Val Asp Ser Glu Glu Gly Leu Leu Ser Thr Gly Arg	80	85	90
Arg Leu Asp Arg Glu Gln Leu Cys Arg Gln Trp Asp Pro Cys Leu	95	100	105
Val Ser Phe Asp Val Leu Ala Thr Gly Asp Leu Ala Leu Ile His	110	115	120
Val Glu Ile Gln Val Leu Asp Ile Asn Asp His Gln Pro Arg Phe	125	130	135
Pro Lys Gly Glu Gln Glu Leu Glu Ile Ser Glu Ser Ala Ser Leu	140	145	150
Arg Thr Arg Ile Pro Leu Asp Arg Ala Leu Asp Pro Asp Thr Gly	155	160	165
Pro Asn Thr Leu His Thr Tyr Thr Leu Ser Pro Ser Glu His Phe	170	175	180
Ala Leu Asp Val Ile Val Gly Pro Asp Glu Thr Lys His Ala Glu	185	190	195
Leu Ile Val Val Lys Glu Leu Asp Arg Glu Ile His Ser Phe Phe	200	205	210
Asp Leu Val Leu Thr Ala Tyr Asp Asn Gly Asn Pro Pro Lys Ser	215	220	225
Gly Thr Ser Leu Val Lys Val Asn Val Leu Asp Ser Asn Asp Asn	230	235	240
Ser Pro Ala Phe Ala Glu Ser Ser Leu Ala Leu Glu Ile Gln Glu	245	250	255
Asp Ala Ala Pro Gly Thr Leu Leu Ile Lys Leu Thr Ala Thr Asp	260	265	270
Pro Asp Gln Gly Pro Asn Gly Glu Val Glu Phe Phe Leu Ser Lys	275	280	285
His Met Pro Pro Glu Val Leu Asp Thr Phe Ser Ile Asp Ala Lys	290	295	300

Thr Gly Gln Val	Ile Leu Arg Arg Pro	Leu Asp Tyr Glu Lys Asn
305	310	315
Pro Ala Tyr Glu	Val Asp Val Gln Ala Arg Asp	Leu Gly Pro Asn
320	325	330
Pro Ile Pro Ala	His Cys Lys Val Leu Ile Lys	Val Leu Asp Val
335	340	345
Asn Asp Asn Ile	Pro Ser Ile His Val Thr Trp	Ala Ser Gln Pro
350	355	360
Ser Leu Val Ser	Glu Ala Leu Pro Lys Asp Ser	Phe Ile Ala Leu
365	370	375
Val Met Ala Asp	Asp Leu Asp Ser Gly His Asn	Gly Leu Val His
380	385	390
Cys Trp Leu Ser	Gln Glu Leu Gly His Phe Arg	Leu Lys Arg Thr
395	400	405
Asn Gly Asn Thr	Tyr Met Leu Leu Thr Asn Ala	Thr Leu Asp Arg
410	415	420
Glu Gln Trp Pro	Lys Tyr Thr Leu Thr Leu Leu	Ala Gln Asp Gln
425	430	435
Gly Leu Gln Pro	Leu Ser Ala Lys Lys Gln Leu	Ser Ile Gln Ile
440	445	450
Ser Asp Ile Asn	Asp Asn Ala Pro Val Phe Glu	Lys Ser Arg Tyr
455	460	465
Glu Val Ser Thr	Arg Glu Asn Asn Leu Pro Ser	Leu His Leu Ile
470	475	480
Thr Ile Lys Ala	His Asp Ala Asp Leu Gly Ile	Asn Gly Lys Val
485	490	495
Ser Tyr Arg Ile	Gln Asp Ser Pro Val Ala His	Leu Val Ala Ile
500	505	510
Asp Ser Asn Thr	Gly Glu Val Thr Ala Gln Arg	Ser Leu Asn Tyr
515	520	525
Glu Glu Met Ala	Gly Phe Glu Phe Gln Val Ile	Ala Glu Asp Ser
530	535	540
Gly Gln Pro Met	Leu Ala Ser Ser Val Ser Val	Trp Val Ser Leu
545	550	555
Leu Asp Ala Asn	Asp Asn Ala Pro Glu Val Val	Gln Pro Val Leu
560	565	570
Ser Asp Gly Lys	Ala Ser Leu Ser Val Leu Val	Asn Ala Ser Thr
575	580	585

Gly His Leu Leu Val	Pro Ile Glu Thr	Pro Asn Gly Leu Gly	Pro
590		595	600
Ala Gly Thr Asp Thr	Pro Pro Leu Ala	Thr His Ser Ser Arg	Pro
605		610	615
Phe Leu Leu Thr Thr	Ile Val Ala Arg	Asp Ala Asp Ser Gly	Ala
620		625	630
Asn Gly Glu Pro Leu	Tyr Ser Ile Arg	Asn Gly Asn Glu Ala	His
635		640	645
Leu Phe Ile Leu Asn	Pro His Thr Gly	Gln Leu Phe Val Asn	Val
650		655	660
Thr Asn Ala Ser Ser	Leu Ile Gly Ser	Glu Trp Glu Leu Glu	Ile
665		670	675
Val Val Glu Asp Gln	Gly Ser Pro Pro	Leu Gln Thr Arg Ala	Leu
680		685	690
Leu Arg Val Met Phe	Val Thr Ser Val	Asp His Leu Arg Asp	Ser
695		700	705
Ala Arg Lys Pro Gly	Ala Leu Ser Met	Ser Met Leu Thr Val	Ile
710		715	720
Cys Leu Ala Val Leu	Leu Gly Ile Phe	Gly Leu Ile Leu Ala	Leu
725		730	735
Phe Met Ser Ile Cys	Arg Thr Glu Lys	Lys Asp Asn Arg Ala	Tyr
740		745	750
Asn Cys Arg Glu Ala	Glu Ser Thr Tyr	Arg Gln Gln Pro Lys	Arg
755		760	765
Pro Gln Lys His Ile	Gln Lys Ala Asp	Ile His Leu Val Pro	Val
770		775	780
Leu Arg Gly Gln Ala	Gly Glu Pro Cys	Glu Val Gly Gln Ser	His
785		790	795
Lys Asp Val Asp Lys	Glu Ala Met Met	Glu Ala Gly Trp Asp	Pro
800		805	810
Cys Leu Gln Ala Pro	Phe His Leu Thr	Pro Thr Leu Tyr Arg	Thr
815		820	825
Leu Arg Asn Gln Gly	Asn Gln Gly Ala	Pro Ala Glu Ser Arg	Glu
830		835	840
Val Leu Gln Asp Thr	Val Asn Leu Leu	Phe Asn His Pro Arg	Gln
845		850	855
Arg Asn Ala Ser Arg	Glu Asn Leu Asn	Leu Pro Glu Pro Gln	Pro
860		865	870

Ala Thr Gly Gln Pro Arg Ser Arg Pro Leu Lys Val Ala Gly Ser	875	880	885
Pro Thr Gly Arg Leu Ala Gly Asp Gln Gly Ser Glu Glu Ala Pro	890	895	900
Gln Arg Pro Pro Ala Ser Ser Ala Thr Leu Arg Arg Gln Arg His	905	910	915
Leu Asn Gly Lys Val Ser Pro Glu Lys Glu Ser Gly Pro Arg Gln	920	925	930
Ile Leu Arg Ser Leu Val Arg Leu Ser Val Ala Ala Phe Ala Glu	935	940	945
Arg Asn Pro Val Glu Glu Leu Thr Val Asp Ser Pro Pro Val Gln	950	955	960
Gln Ile Ser Gln Leu Leu Ser Leu Leu His Gln Gly Gln Phe Gln	965	970	975
Pro Lys Pro Asn His Arg Gly Asn Lys Tyr Leu Ala Lys Pro Gly	980	985	990
Gly Ser Arg Ser Ala Ile Pro Asp Thr Asp Gly Pro Ser Ala Arg	995	1000	1005
Ala Gly Gly Gln Thr Asp Pro Glu Gln Glu Glu Gly Pro Leu Asp	1010	1015	1020
Pro Glu Glu Asp Leu Ser Val Lys Gln Leu Leu Glu Glu Glu Leu	1025	1030	1035
Ser Ser Leu Leu Asp Pro Ser Thr Gly Leu Ala Leu Asp Arg Leu	1040	1045	1050
Ser Ala Pro Asp Pro Ala Trp Met Ala Arg Leu Ser Leu Pro Leu	1055	1060	1065
Thr Thr Asn Tyr Arg Asp Asn Val Ile Ser Pro Asp Ala Ala Ala	1070	1075	1080
Thr Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Ala Glu Ala	1085	1090	1095
Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val	1100	1105	1110
Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser	1115	1120	1125
Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser	1130	1135	1140
Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala	1145	1150	1155

Ser Gly Met Lys Val Gln Gly Asp Pro Gly Gly Lys Thr Gly Thr
1160 1165 1170

Glu Gly Lys Ser Arg Gly Ser Ser Ser Ser Arg Cys Leu
1175 1180

<210> 426

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 426

gtaagcacat gcctccagag gtgc 24

<210> 427

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 427

gtgacgtgga tgcttgggat gttg 24

<210> 428

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 428

tggacacctt cagtattgat gccaagacag gccaggtcat tctgcgtcga 50

<210> 429

<211> 2037

<212> DNA

<213> Homo sapiens

<400> 429

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cctgggagaa ggagaccgt gtgagggggc ctgtggcccc agcgtgctgt 100

ggcctcgggg agtgggaagt ggaggcagga gccttcctta cacttcgcca 150

tgagtttcct catcgactcc agcatcatga ttacctcca gatactat 200

tttggatttg ggtggctttt cttcatgcgc caattgttta aagactatga 250

gatacgtcag tatgtgttac aggtgatctt ctccgtgacg tttgcatttt 300

cttgacccat gtttgagctc atcatctttg aaatcttagg agtattgaat 350
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 aaaaaaaaaa agggcgggccg cgactctaga gtcgacctgc agaagcttgg 2000
 ccgccatggc ccaacttggt tattgcagct tataatg 2037

<210> 430

<211> 455

<212> PRT

<213> Homo sapiens

<400> 430

Met	Ser	Phe	Leu	Ile	Asp	Ser	Ser	Ile	Met	Ile	Thr	Ser	Gln	Ile
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Leu	Phe	Phe	Gly	Phe	Gly	Trp	Leu	Phe	Phe	Met	Arg	Gln	Leu	Phe
				20					25					30
Lys	Asp	Tyr	Glu	Ile	Arg	Gln	Tyr	Val	Val	Gln	Val	Ile	Phe	Ser
				35					40					45
Val	Thr	Phe	Ala	Phe	Ser	Cys	Thr	Met	Phe	Glu	Leu	Ile	Ile	Phe
				50					55					60
Glu	Ile	Leu	Gly	Val	Leu	Asn	Ser	Ser	Ser	Arg	Tyr	Phe	His	Trp
				65					70					75
Lys	Met	Asn	Leu	Cys	Val	Ile	Leu	Leu	Ile	Leu	Val	Phe	Met	Val
				80					85					90
Pro	Phe	Tyr	Ile	Gly	Tyr	Phe	Ile	Val	Ser	Asn	Ile	Arg	Leu	Leu
				95					100					105
His	Lys	Gln	Arg	Leu	Leu	Phe	Ser	Cys	Leu	Leu	Trp	Leu	Thr	Phe
				110					115					120
Met	Tyr	Phe	Phe	Trp	Lys	Leu	Gly	Asp	Pro	Phe	Pro	Ile	Leu	Ser
				125					130					135
Pro	Lys	His	Gly	Ile	Leu	Ser	Ile	Glu	Gln	Leu	Ile	Ser	Arg	Val
				140					145					150
Gly	Val	Ile	Gly	Val	Thr	Leu	Met	Ala	Leu	Leu	Ser	Gly	Phe	Gly
				155					160					165
Ala	Val	Asn	Cys	Pro	Tyr	Thr	Tyr	Met	Ser	Tyr	Phe	Leu	Arg	Asn
				170					175					180
Val	Thr	Asp	Thr	Asp	Ile	Leu	Ala	Leu	Glu	Arg	Arg	Leu	Leu	Gln

185					190					195				
Thr	Met	Asp	Met	Ile	Ile	Ser	Lys	Lys	Lys	Arg	Met	Ala	Met	Ala
				200					205					210
Arg	Arg	Thr	Met	Phe	Gln	Lys	Gly	Glu	Val	His	Asn	Lys	Pro	Ser
				215					220					225
Gly	Phe	Trp	Gly	Met	Ile	Lys	Ser	Val	Thr	Thr	Ser	Ala	Ser	Gly
				230					235					240
Ser	Glu	Asn	Leu	Thr	Leu	Ile	Gln	Gln	Glu	Val	Asp	Ala	Leu	Glu
				245					250					255
Glu	Leu	Ser	Arg	Gln	Leu	Phe	Leu	Glu	Thr	Ala	Asp	Leu	Tyr	Ala
				260					265					270
Thr	Lys	Glu	Arg	Ile	Glu	Tyr	Ser	Lys	Thr	Phe	Lys	Gly	Lys	Tyr
				275					280					285
Phe	Asn	Phe	Leu	Gly	Tyr	Phe	Phe	Ser	Ile	Tyr	Cys	Val	Trp	Lys
				290					295					300
Ile	Phe	Met	Ala	Thr	Ile	Asn	Ile	Val	Phe	Asp	Arg	Val	Gly	Lys
				305					310					315
Thr	Asp	Pro	Val	Thr	Arg	Gly	Ile	Glu	Ile	Thr	Val	Asn	Tyr	Leu
				320					325					330
Gly	Ile	Gln	Phe	Asp	Val	Lys	Phe	Trp	Ser	Gln	His	Ile	Ser	Phe
				335					340					345
Ile	Leu	Val	Gly	Ile	Ile	Ile	Val	Thr	Ser	Ile	Arg	Gly	Leu	Leu
				350					355					360
Ile	Thr	Leu	Thr	Lys	Phe	Phe	Tyr	Ala	Ile	Ser	Ser	Ser	Lys	Ser
				365					370					375
Ser	Asn	Val	Ile	Val	Leu	Leu	Leu	Ala	Gln	Ile	Met	Gly	Met	Tyr
				380					385					390
Phe	Val	Ser	Ser	Val	Leu	Leu	Ile	Arg	Met	Ser	Met	Pro	Leu	Glu
				395					400					405
Tyr	Arg	Thr	Ile	Ile	Thr	Glu	Val	Leu	Gly	Glu	Leu	Gln	Phe	Asn
				410					415					420
Phe	Tyr	His	Arg	Trp	Phe	Asp	Val	Ile	Phe	Leu	Val	Ser	Ala	Leu
				425					430					435
Ser	Ser	Ile	Leu	Phe	Leu	Tyr	Leu	Ala	His	Lys	Gln	Ala	Pro	Glu
				440					445					450
Lys	Gln	Met	Ala	Pro										
				455										

<211> 407
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 78, 81, 113, 157, 224, 297
<223> unknown base

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tggcttttct tcngcgccaa tgtttaaaga ctatgagata cgtcagtatg 150
ttgtacnggt gatcttctcc gtgacgtttg ccatttcttg caccatgttt 200
gagctcatca tctttgaaat cttinggagta ttgaatagca gctcccgta 250
ttttcactgg aaaatgaacc tgtgtgtaat totgctgac ctggttntca 300
tggtgccttt ttacattggc tattttattg tgagcaatat ccgactactg 350
cataaacaac gactgctttt ttctgtctc ttatggctga cctttatgta 400
tttccag 407

<210> 432
<211> 457
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 31, 66, 81-82, 84, 122, 184, 187, 232, 241, 400, 424, 427, 434
<223> unknown base

<400> 432
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tatttttttg atttggggta gnttttttcc atgcgccaat tgtttaaaga 150
ctatgagata cgtcagtatg ttgtacaggt gatnttntcc gtgacgtttg 200
cattttcttg caccatgttt gagctcatca tntttgaaat nttaggagta 250
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tgagcaatat ccgactactg cataaacaac gactgctttt ttctgtctn 400
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cattctc 457

<210> 433

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 433

aagtggagcc ggagccttcc 20

<210> 434

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 434

tcgttggtta tgcagtagtc gg 22

<210> 435

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 435

attgtttaaa gactatgaga tacgtcagta tgttgtagag g 41

<210> 436

<211> 3951

<212> DNA

<213> Homo sapiens

<400> 436

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gggcctccgg gatttgctac ctttttggtt ccctgctcgt cgaactgctc 100

ttctcacggg ctgtgcctt caatctggac gtgatgggtg ccttgcgcaa 150

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gagctgatat gcaaaaggaa agcaaggaga accagtgggtt gggagtcagt 400

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<210> 437
 <211> 1141
 <212> PRT
 <213> Homo sapiens

<400> 437
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 35 40 45
 Gly Glu Pro Gly Ser Leu Phe Gly Phe Ser Val Ala Leu His Arg
 50 55 60
 Gln Leu Gln Pro Arg Pro Gln Ser Trp Leu Leu Val Gly Ala Pro
 65 70 75
 Gln Ala Leu Ala Leu Pro Gly Gln Gln Ala Asn Arg Thr Gly Gly
 80 85 90
 Leu Phe Ala Cys Pro Leu Ser Leu Glu Glu Thr Asp Cys Tyr Arg
 95 100 105

Val Asp Ile Asp Gln Gly Ala Asp Met Gln Lys Glu Ser Lys Glu	110	115	120
Asn Gln Trp Leu Gly Val Ser Val Arg Ser Gln Gly Pro Gly Gly	125	130	135
Lys Ile Val Thr Cys Ala His Arg Tyr Glu Ala Arg Gln Arg Val	140	145	150
Asp Gln Ile Leu Glu Thr Arg Asp Met Ile Gly Arg Cys Phe Val	155	160	165
Leu Ser Gln Asp Leu Ala Ile Arg Asp Glu Leu Asp Gly Gly Glu	170	175	180
Trp Lys Phe Cys Glu Gly Arg Pro Gln Gly His Glu Gln Phe Gly	185	190	195
Phe Cys Gln Gln Gly Thr Ala Ala Ala Phe Ser Pro Asp Ser His	200	205	210
Tyr Leu Leu Phe Gly Ala Pro Gly Thr Tyr Asn Trp Lys Gly Thr	215	220	225
Ala Arg Val Glu Leu Cys Ala Gln Gly Ser Ala Asp Leu Ala His	230	235	240
Leu Asp Asp Gly Pro Tyr Glu Ala Gly Gly Glu Lys Glu Gln Asp	245	250	255
Pro Arg Leu Ile Pro Val Pro Ala Asn Ser Tyr Phe Gly Phe Ser	260	265	270
Ile Asp Ser Gly Lys Gly Leu Val Arg Ala Glu Glu Leu Ser Phe	275	280	285
Val Ala Gly Ala Pro Arg Ala Asn His Lys Gly Ala Val Val Ile	290	295	300
Leu Arg Lys Asp Ser Ala Ser Arg Leu Val Pro Glu Val Met Leu	305	310	315
Ser Gly Glu Arg Leu Thr Ser Gly Phe Gly Tyr Ser Leu Ala Val	320	325	330
Ala Asp Leu Asn Ser Asp Gly Trp Pro Asp Leu Ile Val Gly Ala	335	340	345
Pro Tyr Phe Phe Glu Arg Gln Glu Glu Leu Gly Gly Ala Val Tyr	350	355	360
Val Tyr Leu Asn Gln Gly Gly His Trp Ala Gly Ile Ser Pro Leu	365	370	375
Arg Leu Cys Gly Ser Pro Asp Ser Met Phe Gly Ile Ser Leu Ala	380	385	390

Val Leu Gly Asp	Leu Asn Gln Asp Gly Phe Pro Asp Ile Ala Val	395	400	405
Gly Ala Pro Phe	Asp Gly Asp Gly Lys Val Phe Ile Tyr His Gly	410	415	420
Ser Ser Leu Gly	Val Val Ala Lys Pro Ser Gln Val Leu Glu Gly	425	430	435
Glu Ala Val Gly	Ile Lys Ser Phe Gly Tyr Ser Leu Ser Gly Ser	440	445	450
Leu Asp Met Asp	Gly Asn Gln Tyr Pro Asp Leu Leu Val Gly Ser	455	460	465
Leu Ala Asp Thr	Ala Val Leu Phe Arg Ala Arg Pro Ile Leu His	470	475	480
Val Ser His Glu	Val Ser Ile Ala Pro Arg Ser Ile Asp Leu Glu	485	490	495
Gln Pro Asn Cys	Ala Gly Gly His Ser Val Cys Val Asp Leu Arg	500	505	510
Val Cys Phe Ser	Tyr Ile Ala Val Pro Ser Ser Tyr Ser Pro Thr	515	520	525
Val Ala Leu Asp	Tyr Val Leu Asp Ala Asp Thr Asp Arg Arg Leu	530	535	540
Arg Gly Gln Val	Pro Arg Val Thr Phe Leu Ser Arg Asn Leu Glu	545	550	555
Glu Pro Lys His	Gln Ala Ser Gly Thr Val Trp Leu Lys His Gln	560	565	570
His Asp Arg Val	Cys Gly Asp Ala Met Phe Gln Leu Gln Glu Asn	575	580	585
Val Lys Asp Lys	Leu Arg Ala Ile Val Val Thr Leu Ser Tyr Ser	590	595	600
Leu Gln Thr Pro	Arg Leu Arg Arg Gln Ala Pro Gly Gln Gly Leu	605	610	615
Pro Pro Val Ala	Pro Ile Leu Asn Ala His Gln Pro Ser Thr Gln	620	625	630
Arg Ala Glu Ile	His Phe Leu Lys Gln Gly Cys Gly Glu Asp Lys	635	640	645
Ile Cys Gln Ser	Asn Leu Gln Leu Val His Ala Arg Phe Cys Thr	650	655	660
Arg Val Ser Asp	Thr Glu Phe Gln Pro Leu Pro Met Asp Val Asp	665	670	675

Gly Thr Thr Ala	Leu Phe Ala Leu Ser	Gly Gln Pro Val Ile Gly
680	685	690
Leu Glu Leu Met Val Thr Asn Leu Pro	Ser Asp Pro Ala Gln Pro	
695	700	705
Gln Ala Asp Gly Asp Asp Ala His Glu Ala Gln Leu Leu Val Met		
710	715	720
Leu Pro Asp Ser Leu His Tyr Ser Gly Val Arg Ala Leu Asp Pro		
725	730	735
Ala Glu Lys Pro Leu Cys Leu Ser Asn Glu Asn Ala Ser His Val		
740	745	750
Glu Cys Glu Leu Gly Asn Pro Met Lys Arg Gly Ala Gln Val Thr		
755	760	765
Phe Tyr Leu Ile Leu Ser Thr Ser Gly Ile Ser Ile Glu Thr Thr		
770	775	780
Glu Leu Glu Val Glu Leu Leu Leu Ala Thr Ile Ser Glu Gln Glu		
785	790	795
Leu His Pro Val Ser Ala Arg Ala Arg Val Phe Ile Glu Leu Pro		
800	805	810
Leu Ser Ile Ala Gly Met Ala Ile Pro Gln Gln Leu Phe Phe Ser		
815	820	825
Gly Val Val Arg Gly Glu Arg Ala Met Gln Ser Glu Arg Asp Val		
830	835	840
Gly Ser Lys Val Lys Tyr Glu Val Thr Val Ser Asn Gln Gly Gln		
845	850	855
Ser Leu Arg Thr Leu Gly Ser Ala Phe Leu Asn Ile Met Trp Pro		
860	865	870
His Glu Ile Ala Asn Gly Lys Trp Leu Leu Tyr Pro Met Gln Val		
875	880	885
Glu Leu Glu Gly Gly Gln Gly Pro Gly Gln Lys Gly Leu Cys Ser		
890	895	900
Pro Arg Pro Asn Ile Leu His Leu Asp Val Asp Ser Arg Asp Arg		
905	910	915
Arg Arg Arg Glu Leu Glu Pro Pro Glu Gln Gln Glu Pro Gly Glu		
920	925	930
Arg Gln Glu Pro Ser Met Ser Trp Trp Pro Val Ser Ser Ala Glu		
935	940	945
Lys Lys Lys Asn Ile Thr Leu Asp Cys Ala Arg Gly Thr Ala Asn		
950	955	960

Cys Val Val Phe Ser Cys Pro Leu Tyr Ser Phe Asp Arg Ala Ala	965	970	975
Val Leu His Val Trp Gly Arg Leu Trp Asn Ser Thr Phe Leu Glu	980	985	990
Glu Tyr Ser Ala Val Lys Ser Leu Glu Val Ile Val Arg Ala Asn	995	1000	1005
Ile Thr Val Lys Ser Ser Ile Lys Asn Leu Met Leu Arg Asp Ala	1010	1015	1020
Ser Thr Val Ile Pro Val Met Val Tyr Leu Asp Pro Met Ala Val	1025	1030	1035
Val Ala Glu Gly Val Pro Trp Trp Val Ile Leu Leu Ala Val Leu	1040	1045	1050
Ala Gly Leu Leu Val Leu Ala Leu Leu Val Leu Leu Leu Trp Lys	1055	1060	1065
Met Gly Phe Phe Lys Arg Ala Lys His Pro Glu Ala Thr Val Pro	1070	1075	1080
Gln Tyr His Ala Val Lys Ile Pro Arg Glu Asp Arg Gln Gln Phe	1085	1090	1095
Lys Glu Glu Lys Thr Gly Thr Ile Leu Arg Asn Asn Trp Gly Ser	1100	1105	1110
Pro Arg Arg Glu Gly Pro Asp Ala His Pro Ile Leu Ala Ala Asp	1115	1120	1125
Gly His Pro Glu Leu Gly Pro Asp Gly His Pro Gly Pro Gly Thr	1130	1135	1140

Ala

<210> 438

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 438

ggctgacacc gcagtgtctt tcag 24

<210> 439

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 439

gctgctgggg actgcaatgt agct 24

<210> 440

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 440

catcctccat gtctcccatg aggtctctat tgctccacga agcatc 46

<210> 441

<211> 1964

<212> DNA

<213> Homo sapiens

<400> 441

cgcgccgggc gcaggagct gaggggacgg ctcgagacgg cggcgcgtgc 50

agcagctcca gaaagcagcg agttggcaga gcagggctgc atttccagca 100

ggagctgcga gcacagtgtt ggctcacaac aagatgtctc aggtgtcagc 150

cgtactgtgt gtgtgtgcag ccgcttggtg cagtcagtct ctgcagctg 200

ccgcggcggg ggctgcagcc ggggggcggg cggacggcgg taattttctg 250

gatgataaac aatgggtcac cacaatctct cagtatgaca aggaagtcgg 300

acagtgaac aaattccgag acgaagtaga ggatgattat ttccgcactt 350

ggagtccagg aaaacccttc gatcaggctt tagatccagc taaggatcca 400

tgcttaaaga tgaaatgtag tcgccataaa gtatgcattg ctcaagattc 450

tcagactgca gtctgcatta gtcaccggag gcttacacac aggatgaaag 500

aagcaggagt agaccatagg cagtggaggg gtcccatatt atccacctgc 550

aagcagtgcc cagtggctta tcccagccct gtttgtggtt cagatggtca 600

tacctactct ttccagtgc aactagaata tcaggcatgt gtcttaggaa 650

aacagatctc agtcaaatgt gaaggacatt gcccatgtcc ttccagataag 700

cccaccagta caagcagaaa tgttaagaga gcatgcagtg acctggagtt 750

caggggaagtg gcaaacagat tgcgggactg gttcaaggcc cttcatgaaa 800

gtggaagtca aaacaagaag acaaaaaacat tgctgaggcc tgagagaagc 850

agattcgata ccagcatctt gccaatgtgc aaggactcac ttggctggat 900

gtttaacaga cttgatacaa actatgacct gctattggac cagtcagagc 950
 tcagaagcat ttaccttgat aagaatgaac agtgtaccaa ggcattcttc 1000
 aattcttgtg acacatacaa ggacagttta atatctaata atgagtgggtg 1050
 ctactgcttc cagagacagc aagacccacc ttgccagact gagctcagca 1100
 atattcagaa gcggcaaggg gtaaagaagc tcctaggaca gtatatcccc 1150
 ctgtgtgatg aagatgggta ctacaagcca acacaatgtc atggcagtgt 1200
 tggacagtgc tgggtgtgtg acagatatgg aaatgaagtc atgggatcca 1250
 gaataaatgg tggtgcagat tgtgctatag attttgagat ctccggagat 1300
 tttgctagtg gcgattttca tgaatggact gatgatgagg atgatgaaga 1350
 cgatattatg aatgatgaag atgaaattga agatgatgat gaagatgaag 1400
 gggatgatga tgatgggtgt gatgaccatg atgtatacat ttgattgatg 1450
 acagttgaaa tcaataaatt ctacatttct aatatttaca aaaatgatag 1500
 cctattttaa attatcttct tccccaataa caaaatgatt ctaaacctca 1550
 catatatttt gtataattat ttgaaaaatt gcagctaaag ttatagaact 1600
 ttatgtttaa ataagaatca tttgctttga gtttttatat tccttacaca 1650
 aaaagaaaat acatatgcag tctagtcaga caaaataaag ttttgaagtg 1700
 ctactataat aaatttttca cgagaacaaa ctttgtaaatt cttccataag 1750
 caaaatgaca gctagtgcct gggatcgtag atgttaattt tttgaaagat 1800
 aattctaagt gaaattttaa ataaataaat ttttaatgac ctgggtctta 1850
 aggatttagg aaaaatatgc atgctttaat tgcatttcca aagtagcatc 1900
 ttgctagacc tagatgagtc aggataacag agagatacca catgactcca 1950
 aaaaaaaaaa aaaa 1964

<210> 442

<211> 436

<212> PRT

<213> Homo sapiens

<400> 442

Met	Leu	Lys	Val	Ser	Ala	Val	Leu	Cys	Val	Cys	Ala	Ala	Ala	Trp
1				5				10						15

Cys	Ser	Gln	Ser	Leu	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ala	Ala	Gly
				20				25						30

Gly Arg Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu

35										40					45				
Thr	Thr	Ile	Ser	Gln	Tyr	Asp	Lys	Glu	Val	Gly	Gln	Trp	Asn	Lys					
				50					55					60					
Phe	Arg	Asp	Glu	Val	Glu	Asp	Asp	Tyr	Phe	Arg	Thr	Trp	Ser	Pro					
				65					70					75					
Gly	Lys	Pro	Phe	Asp	Gln	Ala	Leu	Asp	Pro	Ala	Lys	Asp	Pro	Cys					
				80					85					90					
Leu	Lys	Met	Lys	Cys	Ser	Arg	His	Lys	Val	Cys	Ile	Ala	Gln	Asp					
				95					100					105					
Ser	Gln	Thr	Ala	Val	Cys	Ile	Ser	His	Arg	Arg	Leu	Thr	His	Arg					
				110					115					120					
Met	Lys	Glu	Ala	Gly	Val	Asp	His	Arg	Gln	Trp	Arg	Gly	Pro	Ile					
				125					130					135					
Leu	Ser	Thr	Cys	Lys	Gln	Cys	Pro	Val	Val	Tyr	Pro	Ser	Pro	Val					
				140					145					150					
Cys	Gly	Ser	Asp	Gly	His	Thr	Tyr	Ser	Phe	Gln	Cys	Lys	Leu	Glu					
				155					160					165					
Tyr	Gln	Ala	Cys	Val	Leu	Gly	Lys	Gln	Ile	Ser	Val	Lys	Cys	Glu					
				170					175					180					
Gly	His	Cys	Pro	Cys	Pro	Ser	Asp	Lys	Pro	Thr	Ser	Thr	Ser	Arg					
				185					190					195					
Asn	Val	Lys	Arg	Ala	Cys	Ser	Asp	Leu	Glu	Phe	Arg	Glu	Val	Ala					
				200					205					210					
Asn	Arg	Leu	Arg	Asp	Trp	Phe	Lys	Ala	Leu	His	Glu	Ser	Gly	Ser					
				215					220					225					
Gln	Asn	Lys	Lys	Thr	Lys	Thr	Leu	Leu	Arg	Pro	Glu	Arg	Ser	Arg					
				230					235					240					
Phe	Asp	Thr	Ser	Ile	Leu	Pro	Ile	Cys	Lys	Asp	Ser	Leu	Gly	Trp					
				245					250					255					
Met	Phe	Asn	Arg	Leu	Asp	Thr	Asn	Tyr	Asp	Leu	Leu	Leu	Asp	Gln					
				260					265					270					
Ser	Glu	Leu	Arg	Ser	Ile	Tyr	Leu	Asp	Lys	Asn	Glu	Gln	Cys	Thr					
				275					280					285					
Lys	Ala	Phe	Phe	Asn	Ser	Cys	Asp	Thr	Tyr	Lys	Asp	Ser	Leu	Ile					
				290					295					300					
Ser	Asn	Asn	Glu	Trp	Cys	Tyr	Cys	Phe	Gln	Arg	Gln	Gln	Asp	Pro					
				305					310					315					
Pro	Cys	Gln	Thr	Glu	Leu	Ser	Asn	Ile	Gln	Lys	Arg	Gln	Gly	Val					

	320	325	330
Lys Lys Leu Leu Gly Gln Tyr Ile Pro Leu Cys Asp Glu Asp Gly	335	340	345
Tyr Tyr Lys Pro Thr Gln Cys His Gly Ser Val Gly Gln Cys Trp	350	355	360
Cys Val Asp Arg Tyr Gly Asn Glu Val Met Gly Ser Arg Ile Asn	365	370	375
Gly Val Ala Asp Cys Ala Ile Asp Phe Glu Ile Ser Gly Asp Phe	380	385	390
Ala Ser Gly Asp Phe His Glu Trp Thr Asp Asp Glu Asp Asp Glu	395	400	405
Asp Asp Ile Met Asn Asp Glu Asp Glu Ile Glu Asp Asp Asp Glu	410	415	420
Asp Glu Gly Asp Asp Asp Asp Gly Gly Asp Asp His Asp Val Tyr	425	430	435

Ile

<210> 443

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 443

cagcaatatt cagaagcggc aaggg 25

<210> 444

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 444

catcatggtc atcaccacca tcatcatc 28

<210> 445

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 445

ggttactaca agccaacaca atgtcatggc agtggtggac agtgctgg 48

<210> 446

<211> 3617

<212> DNA

<213> Homo sapiens

<400> 446

cagactccag atttccctgt caaccacgag gagtccagag aggaaacgcg 50
gagcggagac aacagtacct gacgcctctt tcagcccggg atcgccccag 100
cagggatggg cgacaagatc tggctgcctt tccccgtgct ccttctggcc 150
gctctgcctc cgggtgctgct gcctggggcg gccggcttca caccttccct 200
cgatagcgac ttcaccttta cccttccgc cgccagaag gagtgcttct 250
accagcccat gcccctgaag gcctcgctgg agatcgagta ccaagtttta 300
gatggagcag gattagatat tgatttccat ctgcctctc cagaaggcaa 350
aaccttagtt tttgaacaaa gaaatcaga tggagttcac actgtagaga 400
ctgaagttgg tgattacatg ttctgctttg acaatacatt cagcaccatt 450
tctgagaagg tgattttctt tgaattaatc ctggataata tgggagaaca 500
ggcacaagaa caagaagatt ggaagaaata tattactggc acagatatat 550
tggatatgaa actggaagac atcctggaat ccatcaacag catcaagtcc 600
agactaagca aaagtgggca catacaaatt ctgcttagag catttgaagc 650
tcgtgatcga aacatacaag aaagcaactt tgatagagtc aatttctggt 700
ctatgggttaa tttagtggtc atgggtggtg tgtcagccat tcaagtttat 750
atgctgaaga gtctgtttga agataagagg aaaagtagaa cttaaaactc 800
caaactagag tacgtaacat tgaaaaatga ggcataaaaa tgcaataaac 850
tgttacagtc aagaccatta atggtcttct ccaaaatatt ttgagatata 900
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tgtgcaagta atcctgctga tccagttgta cttaagtgtg taacaggaat 1000
attttgcaga atataggttt aactgaatga agccatatta ataactgcat 1050
tttcctaact ttgaaaaatt ttgcaaagt cttaggtgat ttaaataaat 1100
gagtattggg cctaattgca acaccagtct gtttttaaca gggtctatta 1150
cccagaactt ttttgtaaat ggggcagtta caaattaact gtggaagttt 1200
tcagttttta gttataaatc acctgagaat tacctaataa tggattgaat 1250

aaatcttttag actacaaaag cccaactttt ctctattttac atatgcatct 1300
ctcctataat gtaaatagaa taatagcttt gaaatacaat taggtttttg 1350
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tagtctttgt actttgctta cattcccaa agctgacatt ttcacgattc 1450
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taaataaata tctccttttc tgagctctaa gaattatcag aaaacaggaa 1800
agaatttaga aaaacttgag aaaaccta ccaaaataaa attcacttaa 1850
gtagaactat aaataaatat ctagaatctg actggctcat catgacatcc 1900
tactcataac ataaatcaaa' ggagatgatt aatttccagt tagctggaag 1950
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 gtacaataat gcacaatcag tgttgctcaa actgctttat acttataaac 3550
 agccatctta aataagcaac gtattgtgag tactgatatg tatataataa 3600
 aaattatcaa aggaaaa 3617

<210> 447

<211> 229

<212> PRT

<213> Homo sapiens

<400> 447

Met	Gly	Asp	Lys	Ile	Trp	Leu	Pro	Phe	Pro	Val	Leu	Leu	Leu	Ala
1				5					10					15

Ala	Leu	Pro	Pro	Val	Leu	Leu	Pro	Gly	Ala	Ala	Gly	Phe	Thr	Pro
				20					25					30

Ser	Leu	Asp	Ser	Asp	Phe	Thr	Phe	Thr	Leu	Pro	Ala	Gly	Gln	Lys
				35					40					45

Glu	Cys	Phe	Tyr	Gln	Pro	Met	Pro	Leu	Lys	Ala	Ser	Leu	Glu	Ile
				50					55					60

Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His	65	70	75
Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe Glu Gln Arg Lys	80	85	90
Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly Asp Tyr Met	95	100	105
Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys Val Ile	110	115	120
Phe Phe Glu Leu Ile Leu Asp Asn Met Gly Glu Gln Ala Gln Glu	125	130	135
Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp	140	145	150
Met Lys Leu Glu Asp Ile Leu Glu Ser Ile Asn Ser Ile Lys Ser	155	160	165
Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu Leu Arg Ala Phe	170	175	180
Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe Asp Arg Val	185	190	195
Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val Val Ser	200	205	210
Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys Arg	215	220	225

Lys Ser Arg Thr

<210> 448

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 448

cccagcaggg ctgggcgaca aga 23

<210> 449

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 449

gtcttccagt ttcatatcca ata 23

<210> 450

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 450

ccagaaggag cacggggaag ggcagccaga tcttgtagcc cat 43

<210> 451

<211> 859

<212> DNA

<213> Homo sapiens

<400> 451

ccatccctga gatcttttta taaaaaaccc agtctttgct gaccagacaa 50

agcataccag atctcaccag agagtcgcag acactatgct gcctcccatg 100

gccctgcccc gtgtgtcctg gatgctgctt tctgcctca ttctcctgtg 150

tcaggttcaa ggtgaagaaa ccagaagga actgccctct ccacggatca 200

gctgtcccaa aggctccaag gcctatggct cccctgcta tgccttgttt 250

ttgtcaccaa aatcctggat ggatgcagat ctggcttgcc agaagcggcc 300

ctctggaaaa ctggtgtctg tgctcagtgg ggctgagggg tccttcgtgt 350

cctccctggg gaggagcatt agtaacagct actcatacat ctggattggg 400

ctccatgacc ccacacaggg ctctgagcct gatggagatg gatgggagtg 450

gagtagcact gatgtgatga attactttgc atgggagaaa aatccctcca 500

ccatcttaaa ccctggccac tgtgggagcc tgtcaagaag cacaggattt 550

ctgaagtgga aagattataa ctgtgatgca aagttaccct atgtctgcaa 600

gttcaaggac tagggcaggt ggggaagtcag cagcctcagc ttggcgtgca 650

gctcatcatg gacatgagac cagtgtgaag actcaccctg gaagagaata 700

ttctcccaa actgccctac ctgactacct tgtcatgac ctccttcttt 750

ttcttttttc ttcaccttca tttcaggctt ttctctgtct tccatgtctt 800

gagatctcag agaataataa taaaaatgtt actttataaa aaaaaaaaaa 850

aaaaaaaaa 859

<210> 452

<211> 175

<212> PRT
<213> Homo sapiens

<400> 452

Met	Leu	Pro	Pro	Met	Ala	Leu	Pro	Ser	Val	Ser	Trp	Met	Leu	Leu	
1				5					10					15	
Ser	Cys	Leu	Ile	Leu	Leu	Cys	Gln	Val	Gln	Gly	Glu	Glu	Thr	Gln	
				20					25					30	
Lys	Glu	Leu	Pro	Ser	Pro	Arg	Ile	Ser	Cys	Pro	Lys	Gly	Ser	Lys	
				35					40					45	
Ala	Tyr	Gly	Ser	Pro	Cys	Tyr	Ala	Leu	Phe	Leu	Ser	Pro	Lys	Ser	
				50					55					60	
Trp	Met	Asp	Ala	Asp	Leu	Ala	Cys	Gln	Lys	Arg	Pro	Ser	Gly	Lys	
				65					70					75	
Leu	Val	Ser	Val	Leu	Ser	Gly	Ala	Glu	Gly	Ser	Phe	Val	Ser	Ser	
				80					85					90	
Leu	Val	Arg	Ser	Ile	Ser	Asn	Ser	Tyr	Ser	Tyr	Ile	Trp	Ile	Gly	
				95					100					105	
Leu	His	Asp	Pro	Thr	Gln	Gly	Ser	Glu	Pro	Asp	Gly	Asp	Gly	Trp	
				110					115					120	
Glu	Trp	Ser	Ser	Thr	Asp	Val	Met	Asn	Tyr	Phe	Ala	Trp	Glu	Lys	
				125					130					135	
Asn	Pro	Ser	Thr	Ile	Leu	Asn	Pro	Gly	His	Cys	Gly	Ser	Leu	Ser	
				140					145					150	
Arg	Ser	Thr	Gly	Phe	Leu	Lys	Trp	Lys	Asp	Tyr	Asn	Cys	Asp	Ala	
				155					160					165	
Lys	Leu	Pro	Tyr	Val	Cys	Lys	Phe	Lys	Asp						
				170					175						

<210> 453

<211> 550

<212> DNA

<213> Homo sapiens

<400> 453

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ggcgctcctg gcgctggtgc tggctgcctg cggagagctg gcgccggccc 150
tgcgctgcta cgtctgtccg gagccacag gagtgtcggg ctgtgtcacc 200
atcgccacct gcaccaccaa cgaaaccatg tgcaagacca cactctactc 250
ccgggagata gtgtaccctt tccaggggga ctccacggtg accaagtcct 300

gtgccagcaa gtgtaagccc tcggatgtgg atggcatcgg ccagaccctg 350
cccgtgtcct gctgcaatac tgagctgtgc aatgtagacg gggcgcccg 400
tctgaacagc ctccactgcg gggccctcac gtcctccca ctcttgagcc 450
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cgaatgcctt gaagaagtgc cccctgcacc aggaaaaaaa aaaaaaaaaa 550

<210> 454
<211> 125
<212> PRT
<213> Homo sapiens

<400> 454
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Cys Gly Glu Leu Ala Pro Ala Leu Arg Cys Tyr Val Cys Pro Glu
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Pro Thr Gly Val Ser Asp Cys Val Thr Ile Ala Thr Cys Thr Thr
35 40 45
Asn Glu Thr Met Cys Lys Thr Thr Leu Tyr Ser Arg Glu Ile Val
50 55 60
Tyr Pro Phe Gln Gly Asp Ser Thr Val Thr Lys Ser Cys Ala Ser
65 70 75
Lys Cys Lys Pro Ser Asp Val Asp Gly Ile Gly Gln Thr Leu Pro
80 85 90
Val Ser Cys Cys Asn Thr Glu Leu Cys Asn Val Asp Gly Ala Pro
95 100 105
Ala Leu Asn Ser Leu His Cys Gly Ala Leu Thr Leu Leu Pro Leu
110 115 120
Leu Ser Leu Arg Leu
125

<210> 455
<211> 1518
<212> DNA
<213> Homo sapiens

<400> 455
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gcgcagcggg agctaccggg gtctttgtcg cgatggtagc ggcggctctc 200

ggcgccacc ctctgctggg agtgagcgcc accttgaact cggttctcaa 250
 ttccaacgct atcaagaacc tgccccacc gctgggcggc gctgcggggc 300
 acccaggctc tgcagtcagc gccgcgccg gaatcctgta cccgggcggg 350
 aataagtacc agaccattga caactaccag ccgtaccctg gcgcagagga 400
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 ctgaaagctt tggtaatgat catagcacct tggatgggta ttccagaaga 650
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 aagcatagga gaaaaggctc tcatggacta gaaatattcc agcgttggtta 850
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 ccttcatcaa ctcaatccta aggatataca agttctgtgg tttcagttaa 1050
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 catttaaaaa aaaaaaaaa 1518

<210> 456

<211> 266

<212> PRT

<213> Homo sapiens

<400> 456

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				20					25					30	
Ala	Thr	Leu	Asn	Ser	Val	Leu	Asn	Ser	Asn	Ala	Ile	Lys	Asn	Leu	
				35					40					45	
Pro	Pro	Pro	Leu	Gly	Gly	Ala	Ala	Gly	His	Pro	Gly	Ser	Ala	Val	
				50					55					60	
Ser	Ala	Ala	Pro	Gly	Ile	Leu	Tyr	Pro	Gly	Gly	Asn	Lys	Tyr	Gln	
				65					70					75	
Thr	Ile	Asp	Asn	Tyr	Gln	Pro	Tyr	Pro	Cys	Ala	Glu	Asp	Glu	Glu	
				80					85					90	
Cys	Gly	Thr	Asp	Glu	Tyr	Cys	Ala	Ser	Pro	Thr	Arg	Gly	Gly	Asp	
				95					100					105	
Ala	Gly	Val	Gln	Ile	Cys	Leu	Ala	Cys	Arg	Lys	Arg	Arg	Lys	Arg	
				110					115					120	
Cys	Met	Arg	His	Ala	Met	Cys	Cys	Pro	Gly	Asn	Tyr	Cys	Lys	Asn	
				125					130					135	
Gly	Ile	Cys	Val	Ser	Ser	Asp	Gln	Asn	His	Phe	Arg	Gly	Glu	Ile	
				140					145					150	
Glu	Glu	Thr	Ile	Thr	Glu	Ser	Phe	Gly	Asn	Asp	His	Ser	Thr	Leu	
				155					160					165	
Asp	Gly	Tyr	Ser	Arg	Arg	Thr	Thr	Leu	Ser	Ser	Lys	Met	Tyr	His	
				170					175					180	
Thr	Lys	Gly	Gln	Glu	Gly	Ser	Val	Cys	Leu	Arg	Ser	Ser	Asp	Cys	
				185					190					195	
Ala	Ser	Gly	Leu	Cys	Cys	Ala	Arg	His	Phe	Trp	Ser	Lys	Ile	Cys	
				200					205					210	
Lys	Pro	Val	Leu	Lys	Glu	Gly	Gln	Val	Cys	Thr	Lys	His	Arg	Arg	
				215					220					225	
Lys	Gly	Ser	His	Gly	Leu	Glu	Ile	Phe	Gln	Arg	Cys	Tyr	Cys	Gly	
				230					235					240	
Glu	Gly	Leu	Ser	Cys	Arg	Ile	Gln	Lys	Asp	His	His	Gln	Ala	Ser	
				245					250					255	
Asn	Ser	Ser	Arg	Leu	His	Thr	Cys	Gln	Arg	His					
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<210> 457
<211> 638
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 30, 123, 133, 139, 180, 214, 259, 282, 308, 452, 467, 471, 473,
509, 556
<223> unknown base

<400> 457
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gcgagcgggg agctaaccgg gttttttgtn gcgatggtag cggcggtttt 200
cggcggccac cttntgctgg gagtgagcgc caccttgaat cggttttcaa 250
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<210> 458
<211> 4040
<212> DNA
<213> Homo sapiens

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cattggaaaag aagagaattt gatgctgctg ttaattctgg agaactgtgg 850
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<210> 459
 <211> 747
 <212> PRT
 <213> Homo sapiens

<400> 459
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 35 40 45
 Ala Ser Ser Arg Glu Ile Arg Gln Ala Phe Lys Lys Leu Ala Leu
 50 55 60
 Lys Leu His Pro Asp Lys Asn Pro Asn Asn Pro Asn Ala His Gly
 65 70 75

Asp Phe Leu Lys Ile Asn Arg Ala Tyr Glu Val Leu Lys Asp Glu	80	85	90
Asp Leu Arg Lys Lys Tyr Asp Lys Tyr Gly Glu Lys Gly Leu Glu	95	100	105
Asp Asn Gln Gly Gly Gln Tyr Glu Ser Trp Asn Tyr Tyr Arg Tyr	110	115	120
Asp Phe Gly Ile Tyr Asp Asp Asp Pro Glu Ile Ile Thr Leu Glu	125	130	135
Arg Arg Glu Phe Asp Ala Ala Val Asn Ser Gly Glu Leu Trp Phe	140	145	150
Val Asn Phe Tyr Ser Pro Gly Cys Ser His Cys His Asp Leu Ala	155	160	165
Pro Thr Trp Arg Asp Phe Ala Lys Glu Val Asp Gly Leu Leu Arg	170	175	180
Ile Gly Ala Val Asn Cys Gly Asp Asp Arg Met Leu Cys Arg Met	185	190	195
Lys Gly Val Asn Ser Tyr Pro Ser Leu Phe Ile Phe Arg Ser Gly	200	205	210
Met Ala Pro Val Lys Tyr His Gly Asp Arg Ser Lys Glu Ser Leu	215	220	225
Val Ser Phe Ala Met Gln His Val Arg Ser Thr Val Thr Glu Leu	230	235	240
Trp Thr Gly Asn Phe Val Asn Ser Ile Gln Thr Ala Phe Ala Ala	245	250	255
Gly Ile Gly Trp Leu Ile Thr Phe Cys Ser Lys Gly Gly Asp Cys	260	265	270
Leu Thr Ser Gln Thr Arg Leu Arg Leu Ser Gly Met Leu Phe Leu	275	280	285
Asn Ser Leu Asp Ala Lys Glu Ile Tyr Leu Glu Val Ile His Asn	290	295	300
Leu Pro Asp Phe Glu Leu Leu Ser Ala Asn Thr Leu Glu Asp Arg	305	310	315
Leu Ala His His Arg Trp Leu Leu Phe Phe His Phe Gly Lys Asn	320	325	330
Glu Asn Ser Asn Asp Pro Glu Leu Lys Lys Leu Lys Thr Leu Leu	335	340	345
Lys Asn Asp His Ile Gln Val Gly Arg Phe Asp Cys Ser Ser Ala	350	355	360

Pro Asp Ile Cys Ser Asn Leu Tyr Val Phe Gln Pro Ser Leu Ala	365	370	375
Val Phe Lys Gly Gln Gly Thr Lys Glu Tyr Glu Ile His His Gly	380	385	390
Lys Lys Ile Leu Tyr Asp Ile Leu Ala Phe Ala Lys Glu Ser Val	395	400	405
Asn Ser His Val Thr Thr Leu Gly Pro Gln Asn Phe Pro Ala Asn	410	415	420
Asp Lys Glu Pro Trp Leu Val Asp Phe Phe Ala Pro Trp Cys Pro	425	430	435
Pro Cys Arg Ala Leu Leu Pro Glu Leu Arg Arg Ala Ser Asn Leu	440	445	450
Leu Tyr Gly Gln Leu Lys Phe Gly Thr Leu Asp Cys Thr Val His	455	460	465
Glu Gly Leu Cys Asn Met Tyr Asn Ile Gln Ala Tyr Pro Thr Thr	470	475	480
Val Val Phe Asn Gln Ser Asn Ile His Glu Tyr Glu Gly His His	485	490	495
Ser Ala Glu Gln Ile Leu Glu Phe Ile Glu Asp Leu Met Asn Pro	500	505	510
Ser Val Val Ser Leu Thr Pro Thr Thr Phe Asn Glu Leu Val Thr	515	520	525
Gln Arg Lys His Asn Glu Val Trp Met Val Asp Phe Tyr Ser Pro	530	535	540
Trp Cys His Pro Cys Gln Val Leu Met Pro Glu Trp Lys Arg Met	545	550	555
Ala Arg Thr Leu Thr Gly Leu Ile Asn Val Gly Ser Ile Asp Cys	560	565	570
Gln Gln Tyr His Ser Phe Cys Ala Gln Glu Asn Val Gln Arg Tyr	575	580	585
Pro Glu Ile Arg Phe Phe Pro Pro Lys Ser Asn Lys Ala Tyr Gln	590	595	600
Tyr His Ser Tyr Asn Gly Trp Asn Arg Asp Ala Tyr Ser Leu Arg	605	610	615
Ile Trp Gly Leu Gly Phe Leu Pro Gln Val Ser Thr Asp Leu Thr	620	625	630
Pro Gln Thr Phe Ser Glu Lys Val Leu Gln Gly Lys Asn His Trp	635	640	645

Val	Ile	Asp	Phe	Tyr	Ala	Pro	Trp	Cys	Gly	Pro	Cys	Gln	Asn	Phe	
				650					655					660	
Ala	Pro	Glu	Phe	Glu	Leu	Leu	Ala	Arg	Met	Ile	Lys	Gly	Lys	Val	
				665					670					675	
Lys	Ala	Gly	Lys	Val	Asp	Cys	Gln	Ala	Tyr	Ala	Gln	Thr	Cys	Gln	
				680					685					690	
Lys	Ala	Gly	Ile	Arg	Ala	Tyr	Pro	Thr	Val	Lys	Phe	Tyr	Phe	Tyr	
				695					700					705	
Glu	Arg	Ala	Lys	Arg	Asn	Phe	Gln	Glu	Glu	Gln	Ile	Asn	Thr	Arg	
				710					715					720	
Asp	Ala	Lys	Ala	Ile	Ala	Ala	Leu	Ile	Ser	Glu	Lys	Leu	Glu	Thr	
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Leu	Arg	Asn	Gln	Gly	Lys	Arg	Asn	Lys	Asp	Glu	Leu				
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 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 460
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<210> 461
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 461
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<210> 462
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 462
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<210> 463
 <211> 1818
 <212> DNA

<213> Homo sapiens

<400> 463

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agaggagaaa atctgtggct ggggagattg ttctcattac tggagctggg 200
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catttaaagg tggacaaaag ctacctccct aaaagtaaata acaaagagaa 1300
cttatttaca caggggaaggt ttaagactgt tcaagtagca ttccaatctg 1350

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 gagatcaagt ttcagcaggc agctttatct caacctggac atattttaag 1450
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 gaattttaag ttctagcccc atgataacct ttttctttgt aatttatgct 1700
 ttcatatatc cttggtccca gagatgttta gacaatttta ggctcaaaaa 1750
 ttaaagctaa cacaggaaaa ggaactgtac tggctattac ataagaaaca 1800
 atggacccaa gagaagaa 1818

<210> 464

<211> 300

<212> PRT

<213> Homo sapiens

<400> 464

Met	Asn	Ile	Ile	Leu	Glu	Ile	Leu	Leu	Leu	Leu	Ile	Thr	Ile	Ile	
1				5					10					15	
Tyr	Ser	Tyr	Leu	Glu	Ser	Leu	Val	Lys	Phe	Phe	Ile	Pro	Gln	Arg	
			20						25					30	
Arg	Lys	Ser	Val	Ala	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	
			35						40					45	
His	Gly	Ile	Gly	Arg	Gln	Thr	Thr	Tyr	Glu	Phe	Ala	Lys	Arg	Gln	
			50						55					60	
Ser	Ile	Leu	Val	Leu	Trp	Asp	Ile	Asn	Lys	Arg	Gly	Val	Glu	Glu	
			65						70					75	
Thr	Ala	Ala	Glu	Cys	Arg	Lys	Leu	Gly	Val	Thr	Ala	His	Ala	Tyr	
			80						85					90	
Val	Val	Asp	Cys	Ser	Asn	Arg	Glu	Glu	Ile	Tyr	Arg	Ser	Leu	Asn	
			95						100					105	
Gln	Val	Lys	Lys	Glu	Val	Gly	Asp	Val	Thr	Ile	Val	Val	Asn	Asn	
			110						115					120	
Ala	Gly	Thr	Val	Tyr	Pro	Ala	Asp	Leu	Leu	Ser	Thr	Lys	Asp	Glu	
			125						130					135	
Glu	Ile	Thr	Lys	Thr	Phe	Glu	Val	Asn	Ile	Leu	Gly	His	Phe	Trp	
			140						145					150	
Ile	Thr	Lys	Ala	Leu	Leu	Pro	Ser	Met	Met	Glu	Arg	Asn	His	Gly	

155	160	165
His Ile Val Thr Val Ala Ser Val Cys Gly	His Glu Gly Ile Pro	
170	175	180
Tyr Leu Ile Pro Tyr Cys Ser Ser Lys Phe	Ala Ala Val Gly Phe	
185	190	195
His Arg Gly Leu Thr Ser Glu Leu Gln Ala	Leu Gly Lys Thr Gly	
200	205	210
Ile Lys Thr Ser Cys Leu Cys Pro Val Phe	Val Asn Thr Gly Phe	
215	220	225
Thr Lys Asn Pro Ser Thr Arg Leu Trp Pro	Val Leu Glu Thr Asp	
230	235	240
Glu Val Val Arg Ser Leu Ile Asp Gly Ile	Leu Thr Asn Lys Lys	
245	250	255
Met Ile Phe Val Pro Ser Tyr Ile Asn Ile	Phe Leu Arg Leu Gln	
260	265	270
Lys Phe Leu Pro Glu Arg Ala Ser Ala Ile	Leu Asn Arg Met Gln	
275	280	285
Asn Ile Gln Phe Glu Ala Val Val Gly His	Lys Ile Lys Met Lys	
290	295	300

<210> 465
 <211> 1547
 <212> DNA
 <213> Homo sapiens

<400> 465
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 gagaggggccc agcccgcccc gggcaggatg accaaggccc ggctgttccg 150
 gctgtggctg gtgctggggg cggtgttcat gatcctgctg atcatcgtgt 200
 actgggacag cgcaggcgcc gcgcacttct acttgcacac gtccttctct 250
 aggccgcaca cggggccgcc gctgcccacg cccggggccgg acagggacag 300
 ggagctcacg gccgactccg atgtcgacga gtttctggac aagtttctca 350
 gtgctggcgt gaagcagagc gaccttccca gaaaggagac ggagcagccg 400
 cctgcgcccg ggagcatgga ggagagcgtg agaggctacg actggtcccc 450
 gcgcgacgcc cggcgcagcc cagaccaggg ccggcagcag gcggagcgga 500
 ggagcgtgct gcggggcttc tgcgccaact ccagcctggc cttccccacc 550

aaggagcgcg cattcgacga catccccaac tcggagctga gccacctgat 600
cgtggacgac cggcacgggg ccatctactg ctacgtgccc aaggtggcct 650
gcaccaactg gaagcgcggtg atgatcgtgc tgagcggaag cctgctgcac 700
cgcggtgcmc cctaccgcmg cccgctgcmc atcccgcmcg agcacgtgca 750
caacgccagc ggcacactga ccttcaacaa gttctggcmc cgctacggga 800
agctctcccg ccacctcatg aaggtcaagc tcaagaagta caccaagttc 850
ctcttcgtgc ggcaccctt cgtgcmctg atctccgct tccgcagcaa 900
gttcgagctg gagaacgagg agttctaccg caagtgcgc gtgcccattg 950
tgcmgtgta cgccaaccac accagcctgc cgcctcggc ggcgaggcc 1000
ttccgcmctg gcctcaaggt gtccttcgcm aacttcatcc agtacctgct 1050
ggaccgcac acggagaagc tggcgccctt caacgagcac tggcggcagg 1100
tgtaccgct ctgccaccg tgccagatcg actacgactt cgtggggaag 1150
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ggaccggcag ctccgcttcc ccccgagcta ccggaacagg accgccagca 1250
gctgggagga ggactggttc gccaatgcc ccctggcctg gaggcagcag 1300
ctgtataaac tctacgaggc cgactttgtt ctcttcggct accccaagcc 1350
cgaaaacctc ctccgagact gaaagcttgc gcgttgcttt ttctcgcmg 1400
cctggaacct gacgcacgc cactccagtt tttttatgac ctacgatttt 1450
gcaatctggg cttctgttc actccactgc ctctatccat tgagtactgt 1500
atcgatattg tttttaaga ttaatatatt tcaggatatt aatacga 1547

<210> 466

<211> 414

<212> PRT

<213> Homo sapiens

<400> 466

Met	Thr	Lys	Ala	Arg	Leu	Phe	Arg	Leu	Trp	Leu	Val	Leu	Gly	Ser
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Val	Phe	Met	Ile	Leu	Leu	Ile	Ile	Val	Tyr	Trp	Asp	Ser	Ala	Gly
				20					25					30

Ala	Ala	His	Phe	Tyr	Leu	His	Thr	Ser	Phe	Ser	Arg	Pro	His	Thr
				35					40					45

Gly	Pro	Pro	Leu	Pro	Thr	Pro	Gly	Pro	Asp	Arg	Asp	Arg	Glu	Leu
				50					55					60

Thr	Ala	Asp	Ser	Asp	Val	Asp	Glu	Phe	Leu	Asp	Lys	Phe	Leu	Ser		65	70	75
Ala	Gly	Val	Lys	Gln	Ser	Asp	Leu	Pro	Arg	Lys	Glu	Thr	Glu	Gln		80	85	90
Pro	Pro	Ala	Pro	Gly	Ser	Met	Glu	Glu	Ser	Val	Arg	Gly	Tyr	Asp		95	100	105
Trp	Ser	Pro	Arg	Asp	Ala	Arg	Arg	Ser	Pro	Asp	Gln	Gly	Arg	Gln		110	115	120
Gln	Ala	Glu	Arg	Arg	Ser	Val	Leu	Arg	Gly	Phe	Cys	Ala	Asn	Ser		125	130	135
Ser	Leu	Ala	Phe	Pro	Thr	Lys	Glu	Arg	Ala	Phe	Asp	Asp	Ile	Pro		140	145	150
Asn	Ser	Glu	Leu	Ser	His	Leu	Ile	Val	Asp	Asp	Arg	His	Gly	Ala		155	160	165
Ile	Tyr	Cys	Tyr	Val	Pro	Lys	Val	Ala	Cys	Thr	Asn	Trp	Lys	Arg		170	175	180
Val	Met	Ile	Val	Leu	Ser	Gly	Ser	Leu	Leu	His	Arg	Gly	Ala	Pro		185	190	195
Tyr	Arg	Asp	Pro	Leu	Arg	Ile	Pro	Arg	Glu	His	Val	His	Asn	Ala		200	205	210
Ser	Ala	His	Leu	Thr	Phe	Asn	Lys	Phe	Trp	Arg	Arg	Tyr	Gly	Lys		215	220	225
Leu	Ser	Arg	His	Leu	Met	Lys	Val	Lys	Leu	Lys	Lys	Tyr	Thr	Lys		230	235	240
Phe	Leu	Phe	Val	Arg	Asp	Pro	Phe	Val	Arg	Leu	Ile	Ser	Ala	Phe		245	250	255
Arg	Ser	Lys	Phe	Glu	Leu	Glu	Asn	Glu	Glu	Phe	Tyr	Arg	Lys	Phe		260	265	270
Ala	Val	Pro	Met	Leu	Arg	Leu	Tyr	Ala	Asn	His	Thr	Ser	Leu	Pro		275	280	285
Ala	Ser	Ala	Arg	Glu	Ala	Phe	Arg	Ala	Gly	Leu	Lys	Val	Ser	Phe		290	295	300
Ala	Asn	Phe	Ile	Gln	Tyr	Leu	Leu	Asp	Pro	His	Thr	Glu	Lys	Leu		305	310	315
Ala	Pro	Phe	Asn	Glu	His	Trp	Arg	Gln	Val	Tyr	Arg	Leu	Cys	His		320	325	330
Pro	Cys	Gln	Ile	Asp	Tyr	Asp	Phe	Val	Gly	Lys	Leu	Glu	Thr	Leu		335	340	345

Asp	Glu	Asp	Ala	Ala	Gln	Leu	Leu	Gln	Leu	Leu	Gln	Val	Asp	Arg	
				350					355					360	
Gln	Leu	Arg	Phe	Pro	Pro	Ser	Tyr	Arg	Asn	Arg	Thr	Ala	Ser	Ser	
				365					370					375	
Trp	Glu	Glu	Asp	Trp	Phe	Ala	Lys	Ile	Pro	Leu	Ala	Trp	Arg	Gln	
				380					385					390	
Gln	Leu	Tyr	Lys	Leu	Tyr	Glu	Ala	Asp	Phe	Val	Leu	Phe	Gly	Tyr	
				395					400					405	
Pro	Lys	Pro	Glu	Asn	Leu	Leu	Arg	Asp							
				410											

<210> 467
 <211> 1071
 <212> DNA
 <213> Homo sapiens

<400> 467
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 acgggatggc tacgggaacg cgctatgccg ggaaggtggg ggtcgtgacc 150
 gggggcgggc gcggcatcgg agctgggatc gtgcgcgcct tcgtgaacag 200
 cggggcccga gtggttatct gcgacaagga tgagtctggg ggccggggccc 250
 tggagcagga gctccctgga gctgtcttta tcctctgtga tgtgactcag 300
 gaagatgatg tgaagaccct ggtttctgag accatccgcc gatttggccg 350
 cctggattgt gttgtcaaca acgctggcca ccaccaccc ccacagaggc 400
 ctgaggagac ctctgcccag ggattccgcc agctgctgga gctgaaccta 450
 ctggggacgt acaccttgac caagctcgcc ctcccctacc tgcggaagag 500
 tcaagggaat gtcacaaaca tctccagcct ggtgggggca atcgccagg 550
 cccaggcagt tccctatgtg gccaccaagg gggcagtaac agccatgacc 600
 aaagctttgg ccctggatga aagtccatat ggtgtccgag tcaactgtat 650
 ctccccagga aacatctgga ccccgctgtg ggaggagctg gcagccttaa 700
 tgccagaccc tagggccaca atccgagagg gcatgctggc ccagccactg 750
 ggccgcatgg gccagccgcg tgaggtcggg gctgcggcag tgttctctggc 800
 ctccgaagcc aacttctgca cgggcattga actgctcgtg acgggggggtg 850
 cagagctggg gtacgggtgc aaggccagtc ggagcacccc cgtggacgcc 900

cccgatatcc cttcctgatt tctctcattt ctacttgggg cccccttcct 950
 aggactctcc caccocaaac tccaacctgt atcagatgca gcccocaagc 1000
 ccttagactc taagcccagt tagcaagggtg ccgggtcacc ctgcagggtc 1050
 ccataaaaaac gatttgcagc c 1071

<210> 468
 <211> 270
 <212> PRT
 <213> Homo sapiens

<400> 468

Met	Ala	Thr	Gly	Thr	Arg	Tyr	Ala	Gly	Lys	Val	Val	Val	Val	Thr	1	5	10	15
Gly	Gly	Gly	Arg	Gly	Ile	Gly	Ala	Gly	Ile	Val	Arg	Ala	Phe	Val	20	25	30	
Asn	Ser	Gly	Ala	Arg	Val	Val	Ile	Cys	Asp	Lys	Asp	Glu	Ser	Gly	35	40	45	
Gly	Arg	Ala	Leu	Glu	Gln	Glu	Leu	Pro	Gly	Ala	Val	Phe	Ile	Leu	50	55	60	
Cys	Asp	Val	Thr	Gln	Glu	Asp	Asp	Val	Lys	Thr	Leu	Val	Ser	Glu	65	70	75	
Thr	Ile	Arg	Arg	Phe	Gly	Arg	Leu	Asp	Cys	Val	Val	Asn	Asn	Ala	80	85	90	
Gly	His	His	Pro	Pro	Pro	Gln	Arg	Pro	Glu	Glu	Thr	Ser	Ala	Gln	95	100	105	
Gly	Phe	Arg	Gln	Leu	Leu	Glu	Leu	Asn	Leu	Leu	Gly	Thr	Tyr	Thr	110	115	120	
Leu	Thr	Lys	Leu	Ala	Leu	Pro	Tyr	Leu	Arg	Lys	Ser	Gln	Gly	Asn	125	130	135	
Val	Ile	Asn	Ile	Ser	Ser	Leu	Val	Gly	Ala	Ile	Gly	Gln	Ala	Gln	140	145	150	
Ala	Val	Pro	Tyr	Val	Ala	Thr	Lys	Gly	Ala	Val	Thr	Ala	Met	Thr	155	160	165	
Lys	Ala	Leu	Ala	Leu	Asp	Glu	Ser	Pro	Tyr	Gly	Val	Arg	Val	Asn	170	175	180	
Cys	Ile	Ser	Pro	Gly	Asn	Ile	Trp	Thr	Pro	Leu	Trp	Glu	Glu	Leu	185	190	195	
Ala	Ala	Leu	Met	Pro	Asp	Pro	Arg	Ala	Thr	Ile	Arg	Glu	Gly	Met	200	205	210	

Leu	Ala	Gln	Pro	Leu	Gly	Arg	Met	Gly	Gln	Pro	Ala	Glu	Val	Gly
				215					220					225
Ala	Ala	Ala	Val	Phe	Leu	Ala	Ser	Glu	Ala	Asn	Phe	Cys	Thr	Gly
				230					235					240
Ile	Glu	Leu	Leu	Val	Thr	Gly	Gly	Ala	Glu	Leu	Gly	Tyr	Gly	Cys
				245					250					255
Lys	Ala	Ser	Arg	Ser	Thr	Pro	Val	Asp	Ala	Pro	Asp	Ile	Pro	Ser
				260					265					270

<210> 469
 <211> 687
 <212> DNA
 <213> Homo sapiens

<400> 469
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 cctcacaacc tgctgtttct tcttaccatt tccatcttcc tggggctggg 100
 ccagcccagg agccccaaaa gcaagaggaa ggggcaagg cggcctgggc 150
 ccctggcccc tggccctcac caggtgccac tggacctggt gtcacgatg 200
 aaaccgtatg cccgcatgga ggagtatgag aggaacatcg aggagatggt 250
 ggcccagctg aggaacagct cagagctggc ccagagaaaag tgtgaggtca 300
 acttgagct gtggatgtcc aacaagagga gcctgtctcc ctggggctac 350
 agcatcaacc acgaccccag ccgtatcccc gtggacctgc cggaggcacg 400
 gtgcctgtgt ctgggctgtg tgaaccctt caccatgcag gaggaccgca 450
 gcatggtgag cgtgccggtg ttcagccagg ttctgtgctg ccgccgcctc 500
 tgcccgccac cgccccgcac agggccttgc cgccagcgcg cagtcatgga 550
 gaccatcgct gtgggctgca cctgcatctt ctgaatcacc tggcccagaa 600
 gccaggccag cagcccagaga ccatcctcct tgcacctttg tgccaagaaa 650
 ggccatgaa aagtaaacac tgacttttga aagcaag 687

<210> 470
 <211> 180
 <212> PRT
 <213> Homo sapiens

<400> 470
 Met Asp Trp Pro His Asn Leu Leu Phe Leu Leu Thr Ile Ser Ile
 1 5 10 15
 Phe Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys
 20 25 30

Gly	Gln	Gly	Arg	Pro	Gly	Pro	Leu	Ala	Pro	Gly	Pro	His	Gln	Val			
				35					40					45			
Pro	Leu	Asp	Leu	Val	Ser	Arg	Met	Lys	Pro	Tyr	Ala	Arg	Met	Glu			
				50					55					60			
Glu	Tyr	Glu	Arg	Asn	Ile	Glu	Glu	Met	Val	Ala	Gln	Leu	Arg	Asn			
				65					70					75			
Ser	Ser	Glu	Leu	Ala	Gln	Arg	Lys	Cys	Glu	Val	Asn	Leu	Gln	Leu			
				80					85					90			
Trp	Met	Ser	Asn	Lys	Arg	Ser	Leu	Ser	Pro	Trp	Gly	Tyr	Ser	Ile			
				95					100					105			
Asn	His	Asp	Pro	Ser	Arg	Ile	Pro	Val	Asp	Leu	Pro	Glu	Ala	Arg			
				110					115					120			
Cys	Leu	Cys	Leu	Gly	Cys	Val	Asn	Pro	Phe	Thr	Met	Gln	Glu	Asp			
				125					130					135			
Arg	Ser	Met	Val	Ser	Val	Pro	Val	Phe	Ser	Gln	Val	Pro	Val	Arg			
				140					145					150			
Arg	Arg	Leu	Cys	Pro	Pro	Pro	Pro	Arg	Thr	Gly	Pro	Cys	Arg	Gln			
				155					160					165			
Arg	Ala	Val	Met	Glu	Thr	Ile	Ala	Val	Gly	Cys	Thr	Cys	Ile	Phe			
				170					175					180			

<210> 471
 <211> 2368
 <212> DNA
 <213> Homo sapiens

<400> 471
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 ctccccgccg agaagcctcg ctgcgcgcc aacatggcgc gtgggcgctg 150
 cggcccgcag ctaacggcgc tctggccgc ctggatcgcg gctgtggcgc 200
 cgacggcagg ccccgaggag gccgcgctgc cgccggagca gagccgggtc 250
 cagcccatga ccgcctccaa ctggacgctg gtgatggagg gcgagtggat 300
 gctgaaattt tacgccccat ggtgtccatc ctgccagcag actgattcag 350
 aatgggaggc ttttgcaaag aatggtgaaa tacttcagat cagtgtgggg 400
 aaggtagatg tcattcaaga accagggttg agtggccgct tctttgtcac 450
 cactctccca gcattttttc atgcaaagga tgggatattc cgccgttattc 500

gtggcccagg aatcttcgaa gacctgcaga attatatctt agagaagaaa 550
tggcaatcag tcgagcctct gactggctgg aaatccccag cttctctaac 600
gatgtctgga atggctggtc ttttagcat ctctggcaag atatggcatc 650
ttcacaaacta tttcacagtg actcttgga ttctgtctg gtgttcttat 700
gtgtttttcg tcatagccac cttggttttt ggccttttta tgggtctggt 750
cttggtgga atatcagaat gttctatgt gccacttcca aggcatttat 800
ctgagcgttc tgagcagaat cggagatcag aggaggctca tagagctgaa 850
cagttgcagg atgcgaggga ggaaaaagat gattcaaatg aagaagaaaa 900
caaagacagc cttgtagatg atgaagaaga gaaagaagat cttggcgatg 950
aggatgaagc agaggaagaa gaggaggagg acaacttggc tgctggtgtg 1000
gatgaggaga gaagtgaggc caatgatcag gggccccag gagaggacgg 1050
tgtgaccgg gaggaagtag agcctgagga ggctgaagaa ggcattctctg 1100
agcaaccctg ccagctgac acagaggtgg tggaagactc cttgaggcag 1150
cgtaaaagtc agcatgctga caagggactg tagatttaat gatgcgtttt 1200
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gtaccaaata ctttaattttt cctgaatgag caagcttctc ttaaaagatg 1300
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agtcttccag gtgtgacaat caggatatag aaaaacaaac gtagtggttg 1400
gatctgtttg gagactggga tgggaacaag ttcatttact taggggtcag 1450
agagtctcga ccagaggagg ccattcccag tcctaatacag caccttccag 1500
agacaaggct gcaggccctg tgaaatgaaa gccaagcagg agccttggct 1550
cctgagcatc cccaaagtgt aacgtagaag cttgcatcc ttttcttggtg 1600
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cagctcagaa gtcatcccag ccctctgaat ctctgtgct atgttttatt 1750
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acactcttca ctattatctc ttggtcagag gactccaata acagccaggt 1850
ttacatgaac tgtgtttgtt cattctgacc taaggggttt agataatcag 1900
taaccataac ccctgaagct gtgactgcca aacatctcaa atgaaatgtt 1950

gtggccatca gagactcaaa aggaagtaag gattttacaa gacagattaa 2000
 aaaaaaattg ttttgtccaa aatatagttg ttgttgattt ttttttaagt 2050
 tttctaagca atatttttca agccagaagt cctctaagtc ttgccagtac 2100
 aaggtagtct tgtgaagaaa agttgaatac tgttttgttt tcatctcaag 2150
 gggttccctg ggtcttgaac tactttaata ataactaaaa aaccacttct 2200
 gattttcctt cagtgatgtg cttttggtga aagaattaat gaactccagt 2250
 acctgaaagt gaaagatttg attttgtttc catcttctgt aatcttccaa 2300
 agaattatat ctttgtaaatt ctctcaatac tcaatctact gtaagtaccc 2350
 agggaggcta atttcttt 2368

<210> 472
 <211> 349
 <212> PRT
 <213> Homo sapiens

<400> 472
 Met Ala Gly Gly Arg Cys Gly Pro Gln Leu Thr Ala Leu Leu Ala
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 Ala Trp Ile Ala Ala Val Ala Ala Thr Ala Gly Pro Glu Glu Ala
 20 25 30
 Ala Leu Pro Pro Glu Gln Ser Arg Val Gln Pro Met Thr Ala Ser
 35 40 45
 Asn Trp Thr Leu Val Met Glu Gly Glu Trp Met Leu Lys Phe Tyr
 50 55 60
 Ala Pro Trp Cys Pro Ser Cys Gln Gln Thr Asp Ser Glu Trp Glu
 65 70 75
 Ala Phe Ala Lys Asn Gly Glu Ile Leu Gln Ile Ser Val Gly Lys
 80 85 90
 Val Asp Val Ile Gln Glu Pro Gly Leu Ser Gly Arg Phe Phe Val
 95 100 105
 Thr Thr Leu Pro Ala Phe Phe His Ala Lys Asp Gly Ile Phe Arg
 110 115 120
 Arg Tyr Arg Gly Pro Gly Ile Phe Glu Asp Leu Gln Asn Tyr Ile
 125 130 135
 Leu Glu Lys Lys Trp Gln Ser Val Glu Pro Leu Thr Gly Trp Lys
 140 145 150
 Ser Pro Ala Ser Leu Thr Met Ser Gly Met Ala Gly Leu Phe Ser
 155 160 165

Ile Ser Gly Lys	Ile Trp His Leu His Asn Tyr Phe Thr Val Thr	170	175	180
Leu Gly Ile Pro	Ala Trp Cys Ser Tyr Val Phe Phe Val Ile Ala	185	190	195
Thr Leu Val Phe	Gly Leu Phe Met Gly Leu Val Leu Val Val Ile	200	205	210
Ser Glu Cys Phe	Tyr Val Pro Leu Pro Arg His Leu Ser Glu Arg	215	220	225
Ser Glu Gln Asn	Arg Arg Ser Glu Glu Ala His Arg Ala Glu Gln	230	235	240
Leu Gln Asp Ala	Glu Glu Glu Lys Asp Asp Ser Asn Glu Glu Glu	245	250	255
Asn Lys Asp Ser	Leu Val Asp Asp Glu Glu Glu Lys Glu Asp Leu	260	265	270
Gly Asp Glu Asp	Glu Ala Glu Glu Glu Glu Glu Glu Asp Asn Leu	275	280	285
Ala Ala Gly Val	Asp Glu Glu Arg Ser Glu Ala Asn Asp Gln Gly	290	295	300
Pro Pro Gly Glu	Asp Gly Val Thr Arg Glu Glu Val Glu Pro Glu	305	310	315
Glu Ala Glu Glu	Gly Ile Ser Glu Gln Pro Cys Pro Ala Asp Thr	320	325	330
Glu Val Val Glu	Asp Ser Leu Arg Gln Arg Lys Ser Gln His Ala	335	340	345
Asp Lys Gly Leu				

<210> 473

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 473

gtccagccca tgaccgcctc caac 24

<210> 474

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 474

ctctcctcat ccacaccagc agcc 24

<210> 475

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 475

gtggatgctg aaattttacg ccccatgggtg tccatcctgc cagc 44

<210> 476

<211> 2478

<212> DNA

<213> Homo sapiens

<400> 476

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gggtaccatg ggggttcttt ccagcccttg tcctcctaata tggattatat 400

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 <211> 201
 <212> PRT
 <213> Homo sapiens

<400> 477

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Val	Ser	Glu	Lys	Gly	Ser	Cys	Ala	Ala	Ser	Pro	Pro	Trp	Arg	Leu	
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Gly	Leu	Ser	Arg	Pro	Gln	Thr	Glu	Val	Pro	Trp	Leu	Trp	Glu	Asp	
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Gly	Ser	Thr	Phe	Ser	Ser	Asn	Leu	Phe	Gln	Ile	Arg	Thr	Thr	Ala	
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Val	Ile	Tyr	Asp	Gln	Leu	Cys	Ser	Val	Pro	Ser	Tyr	Ser	Ile	Cys	
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<400> 479
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<400> 480
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<212> DNA
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 <212> PRT
 <213> Homo sapiens

<400> 483
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 35 40 45
 Leu His Tyr Lys Pro Thr Pro Asp Leu Arg Ile Ser Ile Glu Asn
 50 55 60
 Ser Glu Glu Ala Leu Thr Val His Ala Pro Phe Pro Ala Ala His
 65 70 75
 Pro Ala Ser Arg Ser Phe Pro Asp Pro Arg Gly Leu Tyr His Phe
 80 85 90

Cys	Leu	Tyr	Trp	Asn	Arg	His	Ala	Gly	Arg	Leu	His	Leu	Leu	Tyr	95	100	105
Gly	Lys	Arg	Asp	Phe	Leu	Leu	Ser	Asp	Lys	Ala	Ser	Ser	Leu	Leu	110	115	120
Cys	Phe	Gln	His	Gln	Glu	Glu	Ser	Leu	Ala	Gln	Gly	Pro	Pro	Leu	125	130	135
Leu	Ala	Thr	Ser	Val	Thr	Ser	Trp	Trp	Ser	Pro	Gln	Asn	Ile	Ser	140	145	150
Leu	Pro	Ser	Ala	Ala	Ser	Phe	Thr	Phe	Ser	Phe	His	Ser	Pro	Pro	155	160	165
His	Thr	Ala	Ala	His	Asn	Ala	Ser	Val	Asp	Met	Cys	Glu	Leu	Lys	170	175	180
Arg	Asp	Leu	Gln	Leu	Leu	Ser	Gln	Phe	Leu	Lys	His	Pro	Gln	Lys	185	190	195
Ala	Ser	Arg	Arg	Pro	Ser	Ala	Ala	Pro	Ala	Ser	Gln	Gln	Leu	Gln	200	205	210
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Val	Ser	Phe	Glu	Glu	Asp	Arg	Ile	Asn	Ala	Thr	Val	Trp	Lys	Leu	230	235	240
Gln	Pro	Thr	Ala	Gly	Leu	Gln	Asp	Leu	His	Ile	His	Ser	Arg	Gln	245	250	255
Glu	Glu	Glu	Gln	Ser	Glu	Ile	Met	Glu	Tyr	Ser	Val	Leu	Leu	Pro	260	265	270
Arg	Thr	Leu	Phe	Gln	Arg	Thr	Lys	Gly	Arg	Ser	Gly	Glu	Ala	Glu	275	280	285
Lys	Arg	Leu	Leu	Leu	Val	Asp	Phe	Ser	Ser	Gln	Ala	Leu	Phe	Gln	290	295	300
Asp	Lys	Asn	Ser	Ser	Gln	Val	Leu	Gly	Glu	Lys	Val	Leu	Gly	Ile	305	310	315
Val	Val	Gln	Asn	Thr	Lys	Val	Ala	Asn	Leu	Thr	Glu	Pro	Val	Val	320	325	330
Leu	Thr	Phe	Gln	His	Gln	Leu	Gln	Pro	Lys	Asn	Val	Thr	Leu	Gln	335	340	345
Cys	Val	Phe	Trp	Val	Glu	Asp	Pro	Thr	Leu	Ser	Ser	Pro	Gly	His	350	355	360
Trp	Ser	Ser	Ala	Gly	Cys	Glu	Thr	Val	Arg	Arg	Glu	Thr	Gln	Thr	365	370	375

Ser Cys Phe Cys Asn His Leu Thr Tyr Phe Ala Val Leu Met Val	380	385	390
Ser Ser Val Glu Val Asp Ala Val His Lys His Tyr Leu Ser Leu	395	400	405
Leu Ser Tyr Val Gly Cys Val Val Ser Ala Leu Ala Cys Leu Val	410	415	420
Thr Ile Ala Ala Tyr Leu Cys Ser Arg Val Pro Leu Pro Cys Arg	425	430	435
Arg Lys Pro Arg Asp Tyr Thr Ile Lys Val His Met Asn Leu Leu	440	445	450
Leu Ala Val Phe Leu Leu Asp Thr Ser Phe Leu Leu Ser Glu Pro	455	460	465
Val Ala Leu Thr Gly Ser Glu Ala Gly Cys Arg Ala Ser Ala Ile	470	475	480
Phe Leu His Phe Ser Leu Leu Thr Cys Leu Ser Trp Met Gly Leu	485	490	495
Glu Gly Tyr Asn Leu Tyr Arg Leu Val Val Glu Val Phe Gly Thr	500	505	510
Tyr Val Pro Gly Tyr Leu Leu Lys Leu Ser Ala Met Gly Trp Gly	515	520	525
Phe Pro Ile Phe Leu Val Thr Leu Val Ala Leu Val Asp Val Asp	530	535	540
Asn Tyr Gly Pro Ile Ile Leu Ala Val His Arg Thr Pro Glu Gly	545	550	555
Val Ile Tyr Pro Ser Met Cys Trp Ile Arg Asp Ser Leu Val Ser	560	565	570
Tyr Ile Thr Asn Leu Gly Leu Phe Ser Leu Val Phe Leu Phe Asn	575	580	585
Met Ala Met Leu Ala Thr Met Val Val Gln Ile Leu Arg Leu Arg	590	595	600
Pro His Thr Gln Lys Trp Ser His Val Leu Thr Leu Leu Gly Leu	605	610	615
Ser Leu Val Leu Gly Leu Pro Trp Ala Leu Ile Phe Phe Ser Phe	620	625	630
Ala Ser Gly Thr Phe Gln Leu Val Val Leu Tyr Leu Phe Ser Ile	635	640	645
Ile Thr Ser Phe Gln Gly Phe Leu Ile Phe Ile Trp Tyr Trp Ser	650	655	660

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Ser Arg Ile

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<211> 516

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 68, 70, 84, 147

<223> unknown base

<400> 484

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<210> 485

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 485

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<210> 486

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 486

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<210> 487

<211> 2849

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

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<223> unknown base

<400> 487

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<210> 488

<211> 345

<212> PRT

<213> Homo sapiens

<400> 488

Met	Ser	Leu	Phe	Gly	Leu	Leu	Leu	Leu	Thr	Ser	Ala	Leu	Ala	Gly	1	5	10	15
Gln	Arg	Gln	Gly	Thr	Gln	Ala	Glu	Ser	Asn	Leu	Ser	Ser	Lys	Phe	20	25	30	
Gln	Phe	Ser	Ser	Asn	Lys	Glu	Gln	Asn	Gly	Val	Gln	Asp	Pro	Gln	35	40	45	
His	Glu	Arg	Ile	Ile	Thr	Val	Ser	Thr	Asn	Gly	Ser	Ile	His	Ser	50	55	60	
Pro	Arg	Phe	Pro	His	Thr	Tyr	Pro	Arg	Asn	Thr	Val	Leu	Val	Trp	65	70	75	
Arg	Leu	Val	Ala	Val	Glu	Glu	Asn	Val	Trp	Ile	Gln	Leu	Thr	Phe	80	85	90	
Asp	Glu	Arg	Phe	Gly	Leu	Glu	Asp	Pro	Glu	Asp	Asp	Ile	Cys	Lys	95	100	105	
Tyr	Asp	Phe	Val	Glu	Val	Glu	Glu	Pro	Ser	Asp	Gly	Thr	Ile	Leu	110	115	120	
Gly	Arg	Trp	Cys	Gly	Ser	Gly	Thr	Val	Pro	Gly	Lys	Gln	Ile	Ser	125	130	135	
Lys	Gly	Asn	Gln	Ile	Arg	Ile	Arg	Phe	Val	Ser	Asp	Glu	Tyr	Phe	140	145	150	
Pro	Ser	Glu	Pro	Gly	Phe	Cys	Ile	His	Tyr	Asn	Ile	Val	Met	Pro	155	160	165	

Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu Pro Pro Ser Ala	170	175	180
Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala Phe Ser Thr	185	190	195
Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp Gln Leu	200	205	210
Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly Lys	215	220	225
Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu	230	235	240
Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe	245	250	255
Ser Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe	260	265	270
Trp Pro Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala	275	280	285
Cys Cys Leu His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys	290	295	300
Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr	305	310	315
Gly Val Arg Gly Leu His Lys Ser Leu Thr Asp Val Ala Leu Glu	320	325	330
His His Glu Glu Cys Asp Cys Val Cys Arg Gly Ser Thr Gly Gly	335	340	345

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<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 489

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<210> 490

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 490

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<210> 491

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 491

caccacagcg tttaaccagg 20

<210> 492

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<223> Synthetic oligonucleotide probe

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<210> 495

<211> 3283

<212> DNA

<213> Homo sapiens

<400> 495

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<210> 496

<211> 1049

<212> PRT

<213> Homo sapiens

<400> 496

Met	Val	Phe	Pro	Met	Trp	Thr	Leu	Lys	Arg	Gln	Ile	Leu	Ile	Leu	1	5	10	15
Phe	Asn	Ile	Ile	Leu	Ile	Ser	Lys	Leu	Leu	Gly	Ala	Arg	Trp	Phe	20	25	30	
Pro	Lys	Thr	Leu	Pro	Cys	Asp	Val	Thr	Leu	Asp	Val	Pro	Lys	Asn	35	40	45	
His	Val	Ile	Val	Asp	Cys	Thr	Asp	Lys	His	Leu	Thr	Glu	Ile	Pro	50	55	60	
Gly	Gly	Ile	Pro	Thr	Asn	Thr	Thr	Asn	Leu	Thr	Leu	Thr	Ile	Asn	65	70	75	
His	Ile	Pro	Asp	Ile	Ser	Pro	Ala	Ser	Phe	His	Arg	Leu	Asp	His	80	85	90	
Leu	Val	Glu	Ile	Asp	Phe	Arg	Cys	Asn	Cys	Val	Pro	Ile	Pro	Leu	95	100	105	
Gly	Ser	Lys	Asn	Asn	Met	Cys	Ile	Lys	Arg	Leu	Gln	Ile	Lys	Pro	110	115	120	
Arg	Ser	Phe	Ser	Gly	Leu	Thr	Tyr	Leu	Lys	Ser	Leu	Tyr	Leu	Asp	125	130	135	
Gly	Asn	Gln	Leu	Leu	Glu	Ile	Pro	Gln	Gly	Leu	Pro	Pro	Ser	Leu	140	145	150	
Gln	Leu	Leu	Ser	Leu	Glu	Ala	Asn	Asn	Ile	Phe	Ser	Ile	Arg	Lys	155	160	165	
Glu	Asn	Leu	Thr	Glu	Leu	Ala	Asn	Ile	Glu	Ile	Leu	Tyr	Leu	Gly	170	175	180	
Gln	Asn	Cys	Tyr	Tyr	Arg	Asn	Pro	Cys	Tyr	Val	Ser	Tyr	Ser	Ile	185	190	195	

Glu Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val Leu Ser	200	205	210
Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Val Leu Pro Ser	215	220	225
Thr Leu Thr Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Lys Ile	230	235	240
Gln Glu Asp Asp Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp	245	250	255
Leu Ser Gly Asn Cys Pro Arg Cys Tyr Asn Ala Pro Phe Pro Cys	260	265	270
Ala Pro Cys Lys Asn Asn Ser Pro Leu Gln Ile Pro Val Asn Ala	275	280	285
Phe Asp Ala Leu Thr Glu Leu Lys Val Leu Arg Leu His Ser Asn	290	295	300
Ser Leu Gln His Val Pro Pro Arg Trp Phe Lys Asn Ile Asn Lys	305	310	315
Leu Gln Glu Leu Asp Leu Ser Gln Asn Phe Leu Ala Lys Glu Ile	320	325	330
Gly Asp Ala Lys Phe Leu His Phe Leu Pro Ser Leu Ile Gln Leu	335	340	345
Asp Leu Ser Phe Asn Phe Glu Leu Gln Val Tyr Arg Ala Ser Met	350	355	360
Asn Leu Ser Gln Ala Phe Ser Ser Leu Lys Ser Leu Lys Ile Leu	365	370	375
Arg Ile Arg Gly Tyr Val Phe Lys Glu Leu Lys Ser Phe Asn Leu	380	385	390
Ser Pro Leu His Asn Leu Gln Asn Leu Glu Val Leu Asp Leu Gly	395	400	405
Thr Asn Phe Ile Lys Ile Ala Asn Leu Ser Met Phe Lys Gln Phe	410	415	420
Lys Arg Leu Lys Val Ile Asp Leu Ser Val Asn Lys Ile Ser Pro	425	430	435
Ser Gly Asp Ser Ser Glu Val Gly Phe Cys Ser Asn Ala Arg Thr	440	445	450
Ser Val Glu Ser Tyr Glu Pro Gln Val Leu Glu Gln Leu His Tyr	455	460	465
Phe Arg Tyr Asp Lys Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys	470	475	480

Glu Ala Ser Phe Met Ser Val Asn Glu Ser Cys Tyr Lys Tyr Gly	485	490	495
Gln Thr Leu Asp Leu Ser Lys Asn Ser Ile Phe Phe Val Lys Ser	500	505	510
Ser Asp Phe Gln His Leu Ser Phe Leu Lys Cys Leu Asn Leu Ser	515	520	525
Gly Asn Leu Ile Ser Gln Thr Leu Asn Gly Ser Glu Phe Gln Pro	530	535	540
Leu Ala Glu Leu Arg Tyr Leu Asp Phe Ser Asn Asn Arg Leu Asp	545	550	555
Leu Leu His Ser Thr Ala Phe Glu Glu Leu His Lys Leu Glu Val	560	565	570
Leu Asp Ile Ser Ser Asn Ser His Tyr Phe Gln Ser Glu Gly Ile	575	580	585
Thr His Met Leu Asn Phe Thr Lys Asn Leu Lys Val Leu Gln Lys	590	595	600
Leu Met Met Asn Asp Asn Asp Ile Ser Ser Ser Thr Ser Arg Thr	605	610	615
Met Glu Ser Glu Ser Leu Arg Thr Leu Glu Phe Arg Gly Asn His	620	625	630
Leu Asp Val Leu Trp Arg Glu Gly Asp Asn Arg Tyr Leu Gln Leu	635	640	645
Phe Lys Asn Leu Leu Lys Leu Glu Glu Leu Asp Ile Ser Lys Asn	650	655	660
Ser Leu Ser Phe Leu Pro Ser Gly Val Phe Asp Gly Met Pro Pro	665	670	675
Asn Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu Lys Ser Phe	680	685	690
Ser Trp Lys Lys Leu Gln Cys Leu Lys Asn Leu Glu Thr Leu Asp	695	700	705
Leu Ser His Asn Gln Leu Thr Thr Val Pro Glu Arg Leu Ser Asn	710	715	720
Cys Ser Arg Ser Leu Lys Asn Leu Ile Leu Lys Asn Asn Gln Ile	725	730	735
Arg Ser Leu Thr Lys Tyr Phe Leu Gln Asp Ala Phe Gln Leu Arg	740	745	750
Tyr Leu Asp Leu Ser Ser Asn Lys Ile Gln Met Ile Gln Lys Thr	755	760	765

Ser Phe Pro Glu Asn Val Leu Asn Asn Leu Lys Met Leu Leu Leu	770	775	780
His His Asn Arg Phe Leu Cys Thr Cys Asp Ala Val Trp Phe Val	785	790	795
Trp Trp Val Asn His Thr Glu Val Thr Ile Pro Tyr Leu Ala Thr	800	805	810
Asp Val Thr Cys Val Gly Pro Gly Ala His Lys Gly Gln Ser Val	815	820	825
Ile Ser Leu Asp Leu Tyr Thr Cys Glu Leu Asp Leu Thr Asn Leu	830	835	840
Ile Leu Phe Ser Leu Ser Ile Ser Val Ser Leu Phe Leu Met Val	845	850	855
Met Met Thr Ala Ser His Leu Tyr Phe Trp Asp Val Trp Tyr Ile	860	865	870
Tyr His Phe Cys Lys Ala Lys Ile Lys Gly Tyr Gln Arg Leu Ile	875	880	885
Ser Pro Asp Cys Cys Tyr Asp Ala Phe Ile Val Tyr Asp Thr Lys	890	895	900
Asp Pro Ala Val Thr Glu Trp Val Leu Ala Glu Leu Val Ala Lys	905	910	915
Leu Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys Leu Glu Glu	920	925	930
Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu Ser Gln	935	940	945
Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Asp Lys	950	955	960
Tyr Ala Lys Thr Glu Asn Phe Lys Ile Ala Phe Tyr Leu Ser His	965	970	975
Gln Arg Leu Met Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe	980	985	990
Leu Glu Lys Pro Phe Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys	995	1000	1005
Arg Leu Cys Gly Ser Ser Val Leu Glu Trp Pro Thr Asn Pro Gln	1010	1015	1020
Ala His Pro Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Ala Thr	1025	1030	1035
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<211> 4199
<212> DNA
<213> Homo sapiens

<400> 497
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<210> 498

<211> 1041

<212> PRT

<213> Homo sapiens

<400> 498

Met	Glu	Asn	Met	Phe	Leu	Gln	Ser	Ser	Met	Leu	Thr	Cys	Ile	Phe
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Leu	Leu	Ile	Ser	Gly	Ser	Cys	Glu	Leu	Cys	Ala	Glu	Glu	Asn	Phe
				20					25					30

Ser	Arg	Ser	Tyr	Pro	Cys	Asp	Glu	Lys	Lys	Gln	Asn	Asp	Ser	Val
				35					40					45

Ile	Ala	Glu	Cys	Ser	Asn	Arg	Arg	Leu	Gln	Glu	Val	Pro	Gln	Thr
				50					55					60

Val	Gly	Lys	Tyr	Val	Thr	Glu	Leu	Asp	Leu	Ser	Asp	Asn	Phe	Ile
				65					70					75

Thr	His	Ile	Thr	Asn	Glu	Ser	Phe	Gln	Gly	Leu	Gln	Asn	Leu	Thr
				80					85					90

Lys	Ile	Asn	Leu	Asn	His	Asn	Pro	Asn	Val	Gln	His	Gln	Asn	Gly
				95					100					105

Asn	Pro	Gly	Ile	Gln	Ser	Asn	Gly	Leu	Asn	Ile	Thr	Asp	Gly	Ala
				110					115					120

Phe	Leu	Asn	Leu	Lys	Asn	Leu	Arg	Glu	Leu	Leu	Leu	Glu	Asp	Asn
				125					130					135

Gln	Leu	Pro	Gln	Ile	Pro	Ser	Gly	Leu	Pro	Glu	Ser	Leu	Thr	Glu
				140					145					150

Leu	Ser	Leu	Ile	Gln	Asn	Asn	Ile	Tyr	Asn	Ile	Thr	Lys	Glu	Gly
				155					160					165

Ile	Ser	Arg	Leu	Ile	Asn	Leu	Lys	Asn	Leu	Tyr	Leu	Ala	Trp	Asn
				170					175					180

Cys	Tyr	Phe	Asn	Lys	Val	Cys	Glu	Lys	Thr	Asn	Ile	Glu	Asp	Gly
				185					190					195

Val	Phe	Glu	Thr	Leu	Thr	Asn	Leu	Glu	Leu	Leu	Ser	Leu	Ser	Phe
				200					205					210

Asn	Ser	Leu	Ser	His	Val	Pro	Pro	Lys	Leu	Pro	Ser	Ser	Leu	Arg
				215					220					225

Lys	Leu	Phe	Leu	Ser	Asn	Thr	Gln	Ile	Lys	Tyr	Ile	Ser	Glu	Glu
				230					235					240

Asp Phe Lys Gly	Leu Ile Asn Leu Thr	Leu Leu Asp Leu Ser	Gly
245	250		255
Asn Cys Pro Arg	Cys Phe Asn Ala Pro	Phe Pro Cys Val Pro	Cys
260	265		270
Asp Gly Gly Ala	Ser Ile Asn Ile Asp	Arg Phe Ala Phe Gln	Asn
275	280		285
Leu Thr Gln Leu	Arg Tyr Leu Asn Leu	Ser Ser Thr Ser Leu	Arg
290	295		300
Lys Ile Asn Ala	Ala Trp Phe Lys Asn	Met Pro His Leu Lys	Val
305	310		315
Leu Asp Leu Glu	Phe Asn Tyr Leu Val	Gly Glu Ile Val Ser	Gly
320	325		330
Ala Phe Leu Thr	Met Leu Pro Arg Leu	Glu Ile Leu Asp Leu	Ser
335	340		345
Phe Asn Tyr Ile	Lys Gly Ser Tyr Pro	Gln His Ile Asn Ile	Ser
350	355		360
Arg Asn Phe Ser	Lys Leu Leu Ser Leu	Arg Ala Leu His Leu	Arg
365	370		375
Gly Tyr Val Phe	Gln Glu Leu Arg Glu	Asp Asp Phe Gln Pro	Leu
380	385		390
Met Gln Leu Pro	Asn Leu Ser Thr Ile	Asn Leu Gly Ile Asn	Phe
395	400		405
Ile Lys Gln Ile	Asp Phe Lys Leu Phe	Gln Asn Phe Ser Asn	Leu
410	415		420
Glu Ile Ile Tyr	Leu Ser Glu Asn Arg	Ile Ser Pro Leu Val	Lys
425	430		435
Asp Thr Arg Gln	Ser Tyr Ala Asn Ser	Ser Ser Phe Gln Arg	His
440	445		450
Ile Arg Lys Arg	Arg Ser Thr Asp Phe	Glu Phe Asp Pro His	Ser
455	460		465
Asn Phe Tyr His	Phe Thr Arg Pro Leu	Ile Lys Pro Gln Cys	Ala
470	475		480
Ala Tyr Gly Lys	Ala Leu Asp Leu Ser	Leu Asn Ser Ile Phe	Phe
485	490		495
Ile Gly Pro Asn	Gln Phe Glu Asn Leu	Pro Asp Ile Ala Cys	Leu
500	505		510
Asn Leu Ser Ala	Asn Ser Asn Ala Gln	Val Leu Ser Gly Thr	Glu
515	520		525

Phe Ser Ala Ile	Pro His Val Lys Tyr	Leu Asp Leu Thr	Asn Asn
530		535	540
Arg Leu Asp Phe	Asp Asn Ala Ser Ala	Leu Thr Glu Leu Ser	Asp
545		550	555
Leu Glu Val Leu	Asp Leu Ser Tyr Asn	Ser His Tyr Phe Arg	Ile
560		565	570
Ala Gly Val Thr	His His Leu Glu Phe	Ile Gln Asn Phe Thr	Asn
575		580	585
Leu Lys Val Leu	Asn Leu Ser His Asn	Asn Ile Tyr Thr Leu Thr	
590		595	600
Asp Lys Tyr Asn	Leu Glu Ser Lys Ser	Leu Val Glu Leu Val Phe	
605		610	615
Ser Gly Asn Arg	Leu Asp Ile Leu Trp	Asn Asp Asp Asp Asn Arg	
620		625	630
Tyr Ile Ser Ile	Phe Lys Gly Leu Lys	Asn Leu Thr Arg Leu Asp	
635		640	645
Leu Ser Leu Asn	Arg Leu Lys His Ile	Pro Asn Glu Ala Phe Leu	
650		655	660
Asn Leu Pro Ala	Ser Leu Thr Glu Leu	His Ile Asn Asp Asn Met	
665		670	675
Leu Lys Phe Phe	Asn Trp Thr Leu Leu	Gln Gln Phe Pro Arg Leu	
680		685	690
Glu Leu Leu Asp	Leu Arg Gly Asn Lys	Leu Leu Phe Leu Thr Asp	
695		700	705
Ser Leu Ser Asp	Phe Thr Ser Ser Leu	Arg Thr Leu Leu Leu Ser	
710		715	720
His Asn Arg Ile	Ser His Leu Pro Ser	Gly Phe Leu Ser Glu Val	
725		730	735
Ser Ser Leu Lys	His Leu Asp Leu Ser	Ser Asn Leu Leu Lys Thr	
740		745	750
Ile Asn Lys Ser	Ala Leu Glu Thr Lys	Thr Thr Thr Lys Leu Ser	
755		760	765
Met Leu Glu Leu	His Gly Asn Pro Phe	Glu Cys Thr Cys Asp Ile	
770		775	780
Gly Asp Phe Arg	Arg Trp Met Asp Glu	His Leu Asn Val Lys Ile	
785		790	795
Pro Arg Leu Val	Asp Val Ile Cys Ala	Ser Pro Gly Asp Gln Arg	
800		805	810

Gly Lys Ser Ile Val Ser Leu Glu Leu Thr Thr Cys Val Ser Asp	815	820	825
Val Thr Ala Val Ile Leu Phe Phe Phe Thr Phe Phe Ile Thr Thr	830	835	840
Met Val Met Leu Ala Ala Leu Ala His His Leu Phe Tyr Trp Asp	845	850	855
Val Trp Phe Ile Tyr Asn Val Cys Leu Ala Lys Val Lys Gly Tyr	860	865	870
Arg Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser	875	880	885
Tyr Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu	890	895	900
Leu Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu	905	910	915
Cys Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp	920	925	930
Asn Leu Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val	935	940	945
Leu Thr Lys Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe	950	955	960
Tyr Leu Ala Leu Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile	965	970	975
Ile Phe Ile Leu Leu Glu Pro Val Leu Gln His Ser Gln Tyr Leu	980	985	990
Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile Leu Gln Trp Pro	995	1000	1005
Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp Gln Thr Leu Arg Asn	1010	1015	1020
Val Val Leu Thr Glu Asn Asp Ser Arg Tyr Asn Asn Met Tyr Val	1025	1030	1035
Asp Ser Ile Lys Gln Tyr	1040		

<210> 499

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 500
<211> 20
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 500
atccatgagc ctctgatggg 20

<210> 501
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 502
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 502
gccgagacaa aaacgttctc c 21

<210> 503
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 503
catccatggt ctcattcatt agcc 24

<210> 504
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 504
tcgacaacct catgcagagc atcaacacaaa gcaagaaaac agtatt 46

<210> 505

<211> 1738

<212> DNA

<213> Homo sapiens

<400> 505

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ggctgcaagg gaggtcctg tggacaggcc aggcaggtgg gcctcaggag 150
gtgcctccag gcggccagt ggctgaggc ccagcaagg gctagggctc 200
atctccagtc ccaggacaca gcagcggcca ccatggccac gcctgggctc 250
cagcagcatc agcagcccc aggaccggg aggcacaggt ggccccacc 300
accggagga gcagctcctg cccctgtccg ggggatgact gattctctc 350
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gaggggctct caggaggtgc tgctgatgtg gcttctggtg ttggcagtgg 450
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gtcacgggg accctgtctc cgagtcgttc gtgcagcgtg tgtaccagcc 550
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tccagcctgg ccgtgccgc tgccctgcag gatggcgggg tgacacttgc 800
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aatgaaacgt gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650
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gcccaacttg tttattgcag cttataatgg ttacaaat 1738

<210> 506

<211> 273

<212> PRT

<213> Homo sapiens

<400> 506

Met	Arg	Gly	Ser	Gln	Glu	Val	Leu	Leu	Met	Trp	Leu	Leu	Val	Leu
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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25					30
Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35					40					45
Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg
				50					55					60
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg
				65					70					75
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro
				80					85					90
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala
				95					100					105
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro
				110					115					120
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln
				125					130					135
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln
				140					145					150
Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu

	155		160		165
Gly His Ser Leu	Ser Ala Asp Gly Thr	Leu Cys Val Pro Lys	Gly		
	170		175		180
Gly Pro Pro Arg	Val Ala Pro Asn Pro	Thr Gly Val Asp Ser	Ala		
	185		190		195
Met Lys Glu Glu	Val Gln Arg Leu Gln	Ser Arg Val Asp Leu	Leu		
	200		205		210
Glu Glu Lys Leu	Gln Leu Val Leu Ala	Pro Leu His Ser Leu	Ala		
	215		220		225
Ser Gln Ala Leu	Glu His Gly Leu Pro	Asp Pro Gly Ser Leu	Leu		
	230		235		240
Val His Ser Phe	Gln Gln Leu Gly Arg	Ile Asp Ser Leu Ser	Glu		
	245		250		255
Gln Ile Ser Phe	Leu Glu Glu Gln Leu	Gly Ser Cys Ser Cys	Lys		
	260		265		270

Lys Asp Ser

<210> 507
 <211> 1700
 <212> DNA
 <213> Homo sapiens

<400> 507
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 tggatgagca acccaacggg ggcccgggga ggggaactgg ccccagggga 300
 gaggaacccc aaagccacat ctgtagccag gatgagcagt gtgaatccag 350
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 cacgcctacc ggcccggccg tagggtgtgt gctgtccggg ctcacgggga 600
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cctgcgacgg gcaccggggc tgcagcacct accgaaccat ctataggacc 700
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<210> 508

<211> 273

<212> PRT

<213> Homo sapiens

<400> 508

Met	Arg	Gly	Ser	Gln	Glu	Val	Leu	Leu	Met	Trp	Leu	Leu	Val	Leu
1					5				10					15

Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25					30

Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35					40					45

Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg	
				50						55				60	
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	
				65					70					75	
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	
				80					85					90	
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	
				95					100					105	
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro	
				110					115					120	
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln	
				125					130					135	
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln	
				140					145					150	
Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu	
				155					160					165	
Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Pro	Lys	Gly	
				170					175					180	
Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	Asp	Ser	Ala	
				185					190					195	
Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	Leu	Leu	
				200					205					210	
Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala	
				215					220					225	
Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu	
				230					235					240	
Val	His	Ser	Phe	Gln	Gln	Leu	Gly	Arg	Ile	Asp	Ser	Leu	Ser	Glu	
				245					250					255	
Gln	Ile	Ser	Phe	Leu	Glu	Glu	Gln	Leu	Gly	Ser	Cys	Ser	Cys	Lys	
				260					265					270	

Lys Asp Ser

<210> 509

<211> 1538

<212> DNA

<213> Homo sapiens

<400> 509

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ggggccacca tggccacgcc tgggtccag cagcatcagc agccccagg 200
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<210> 510

<211> 273

<212> PRT

<213> Homo sapiens

<400> 510

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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25					30

Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35					40					45

Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg
				50					55					60

Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg
				65					70					75

Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro
				80					85					90

Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala
				95					100					105

Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro
				110					115					120

Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln
				125					130					135

Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln
				140					145					150

Arg	Cys	Val	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu
				155					160					165

Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Pro	Lys	Gly
				170					175					180

Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	Asp	Ser	Ala
				185					190					195

Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	Leu	Leu
				200					205					210

Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala
				215					220					225

Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu
				230					235					240

Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu
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Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys
260 265 270

Lys Asp Ser

<210> 511

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 511

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<210> 512

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 512

ttttccactc ctgtcgggtt gg 22

<210> 513

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 513

ggtgacactt gccagtcaga tgtggatgaa tgcagtgcta ggaggg 46

<210> 514

<211> 2690

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2039-2065

<223> unknown base

<400> 514

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<210> 515

<211> 364

<212> PRT

<213> Homo sapiens.

<400> 515

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	20	25	30
Met Ala Arg Gln Lys Gly Ile Phe Tyr Leu Thr Leu Phe Leu Ile	35	40	45
Leu Gly Thr Cys Thr Leu Phe Phe Ala Phe Glu Cys Arg Tyr Leu	50	55	60
Ala Val Gln Leu Ser Pro Ala Ile Pro Val Phe Ala Ala Met Leu	65	70	75
Phe Leu Phe Ser Met Ala Thr Leu Leu Arg Thr Ser Phe Ser Asp	80	85	90
Pro Gly Val Ile Pro Arg Ala Leu Pro Asp Glu Ala Ala Phe Ile	95	100	105
Glu Met Glu Ile Glu Ala Thr Asn Gly Ala Val Pro Gln Gly Gln	110	115	120
Arg Pro Pro Pro Arg Ile Lys Asn Phe Gln Ile Asn Asn Gln Ile	125	130	135
Val Lys Leu Lys Tyr Cys Tyr Thr Cys Lys Ile Phe Arg Pro Pro	140	145	150
Arg Ala Ser His Cys Ser Ile Cys Asp Asn Cys Val Glu Arg Phe	155	160	165
Asp His His Cys Pro Trp Val Gly Asn Cys Val Gly Lys Arg Asn	170	175	180
Tyr Arg Tyr Phe Tyr Leu Phe Ile Leu Ser Leu Ser Leu Leu Thr	185	190	195
Ile Tyr Val Phe Ala Phe Asn Ile Val Tyr Val Ala Leu Lys Ser	200	205	210
Leu Lys Ile Gly Phe Leu Glu Thr Leu Lys Glu Thr Pro Gly Thr	215	220	225
Val Leu Glu Val Leu Ile Cys Phe Phe Thr Leu Trp Ser Val Val	230	235	240
Gly Leu Thr Gly Phe His Thr Phe Leu Val Ala Leu Asn Gln Thr	245	250	255
Thr Asn Glu Asp Ile Lys Gly Ser Trp Thr Gly Lys Asn Arg Val	260	265	270
Gln Asn Pro Tyr Ser His Gly Asn Ile Val Lys Asn Cys Cys Glu	275	280	285
Val Leu Cys Gly Pro Leu Pro Pro Ser Val Leu Asp Arg Arg Gly	290	295	300
Ile Leu Pro Leu Glu Glu Ser Gly Ser Arg Pro Pro Ser Thr Gln			

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Glu Thr Ser Ser Ser Leu Leu Pro Gln Ser Pro Ala Pro Thr Glu					
	320		325		330
His Leu Asn Ser Asn Glu Met Pro Glu Asp Ser Ser Thr Pro Glu					
	335		340		345
Glu Met Pro Pro Pro Glu Pro Pro Glu Pro Pro Gln Glu Ala Ala					
	350		355		360
Glu Ala Glu Lys					

<210> 516
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 36, 38, 88, 118, 135, 193, 213, 222
 <223> unknown base

<400> 516
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 cccctgggtg gggaattgtg ttggaaagag gaactaccgc tanttctacc 200
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 atcgt 255

<210> 517
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 517
 caacgtgatt tcaaagctgg gctc 24

<210> 518
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 518

gcctcgatc aagaatttcc 20

<210> 519

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519

agtggaagtc gacctccc 18

<210> 520

<211> 24

<212> DNA

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<223> Synthetic oligonucleotide probe

<400> 520

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<210> 521

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 521

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<210> 522

<211> 1679

<212> DNA

<213> Homo sapiens

<400> 522

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agagcaacac aatctatcag gaaagaaaga aagaaaaaaa ccgaacctga 100

caaaaaagaa gaaaaagaag aagaaaaaaa atcatgaaaa ccatccagcc 150

aaaaatgcac aattctatct cttgggcaat cttcacgggg ctggctgctc 200

tgtgtctctt ccaaggagtgc ccggtgcgca gcggagatgc caccttcccc 250

aaagctatgg acaacgtgac ggtccggcag ggggagagcg ccaccctcag 300

gtgcactatt gacaaccggg tcaccggggt ggcttggtta aaccgcagca 350

ccatcctcta tgctgggaat gacaagtggg gcctggatcc tcgctgggtc 400

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<210> 523

<211> 344

<212> PRT

<213> Homo sapiens

<400> 523

Met	Lys	Thr	Ile	Gln	Pro	Lys	Met	His	Asn	Ser	Ile	Ser	Trp	Ala	
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Ile	Phe	Thr	Gly	Leu	Ala	Ala	Leu	Cys	Leu	Phe	Gln	Gly	Val	Pro	
				20					25					30	
Val	Arg	Ser	Gly	Asp	Ala	Thr	Phe	Pro	Lys	Ala	Met	Asp	Asn	Val	
				35					40					45	
Thr	Val	Arg	Gln	Gly	Glu	Ser	Ala	Thr	Leu	Arg	Cys	Thr	Ile	Asp	
				50					55					60	
Asn	Arg	Val	Thr	Arg	Val	Ala	Trp	Leu	Asn	Arg	Ser	Thr	Ile	Leu	
				65					70					75	
Tyr	Ala	Gly	Asn	Asp	Lys	Trp	Cys	Leu	Asp	Pro	Arg	Val	Val	Leu	
				80					85					90	
Leu	Ser	Asn	Thr	Gln	Thr	Gln	Tyr	Ser	Ile	Glu	Ile	Gln	Asn	Val	
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Asp	Val	Tyr	Asp	Glu	Gly	Pro	Tyr	Thr	Cys	Ser	Val	Gln	Thr	Asp	
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Asn	His	Pro	Lys	Thr	Ser	Arg	Val	His	Leu	Ile	Val	Gln	Val	Ser	
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Pro	Lys	Ile	Val	Glu	Ile	Ser	Ser	Asp	Ile	Ser	Ile	Asn	Glu	Gly	
				140					145					150	
Asn	Asn	Ile	Ser	Leu	Thr	Cys	Ile	Ala	Thr	Gly	Arg	Pro	Glu	Pro	
				155					160					165	
Thr	Val	Thr	Trp	Arg	His	Ile	Ser	Pro	Lys	Ala	Val	Gly	Phe	Val	
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Ser	Glu	Asp	Glu	Tyr	Leu	Glu	Ile	Gln	Gly	Ile	Thr	Arg	Glu	Gln	
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Ser	Gly	Asp	Tyr	Glu	Cys	Ser	Ala	Ser	Asn	Asp	Val	Ala	Ala	Pro	
				200					205					210	
Val	Val	Arg	Arg	Val	Lys	Val	Thr	Val	Asn	Tyr	Pro	Pro	Tyr	Ile	
				215					220					225	
Ser	Glu	Ala	Lys	Gly	Thr	Gly	Val	Pro	Val	Gly	Gln	Lys	Gly	Thr	
				230					235					240	
Leu	Gln	Cys	Glu	Ala	Ser	Ala	Val	Pro	Ser	Ala	Glu	Phe	Gln	Trp	
				245					250					255	
Tyr	Lys	Asp	Asp	Lys	Arg	Leu	Ile	Glu	Gly	Lys	Lys	Gly	Val	Lys	
				260					265					270	
Val	Glu	Asn	Arg	Pro	Phe	Leu	Ser	Lys	Leu	Ile	Phe	Phe	Asn	Val	
				275					280					285	

Ser Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys
290 295 300

Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala
305 310 315

Val Ser Glu Val Ser Asn Gly Thr Ser Arg Arg Ala Gly Cys Val
320 325 330

Trp Leu Leu Pro Leu Leu Val Leu His Leu Leu Leu Lys Phe
335 340

<210> 524

<211> 503

<212> DNA

<213> Homo sapiens

<400> 524

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<211> 2602

<212> DNA

<213> Homo sapiens

<400> 525

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<211> 736

<212> PRT

<213> Homo sapiens

<400> 526

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Glu	Leu	Val	Leu	Ala	Gly	Ala	Ser	Leu	Leu	Leu	Ala	Ala	Leu	Leu
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Leu	Gly	Cys	Leu	Val	Ala	Leu	Gly	Val	Gln	Tyr	His	Arg	Asp	Pro
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Ser His Ser Thr Cys Leu Thr Glu Ala Cys Ile Arg Val Ala Gly	65	70	75
Lys Ile Leu Glu Ser Leu Asp Arg Gly Val Ser Pro Cys Glu Asp	80	85	90
Phe Tyr Gln Phe Ser Cys Gly Gly Trp Ile Arg Arg Asn Pro Leu	95	100	105
Pro Asp Gly Arg Ser Arg Trp Asn Thr Phe Asn Ser Leu Trp Asp	110	115	120
Gln Asn Gln Ala Ile Leu Lys His Leu Leu Glu Asn Thr Thr Phe	125	130	135
Asn Ser Ser Ser Glu Ala Glu Gln Lys Thr Gln Arg Phe Tyr Leu	140	145	150
Ser Cys Leu Gln Val Glu Arg Ile Glu Glu Leu Gly Ala Gln Pro	155	160	165
Leu Arg Asp Leu Ile Glu Lys Ile Gly Gly Trp Asn Ile Thr Gly	170	175	180
Pro Trp Asp Gln Asp Asn Phe Met Glu Val Leu Lys Ala Val Ala	185	190	195
Gly Thr Tyr Arg Ala Thr Pro Phe Phe Thr Val Tyr Ile Ser Ala	200	205	210
Asp Ser Lys Ser Ser Asn Ser Asn Val Ile Gln Val Asp Gln Ser	215	220	225
Gly Leu Phe Leu Pro Ser Arg Asp Tyr Tyr Leu Asn Arg Thr Ala	230	235	240
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Gly Met Leu Leu Gly Gly Arg Pro Thr Ser Thr Arg Glu Gln Met	260	265	270
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Pro Gln Asp Gln Arg Arg Asp Glu Glu Lys Ile Tyr His Lys Met	290	295	300
Ser Ile Ser Glu Leu Gln Ala Leu Ala Pro Ser Met Asp Trp Leu	305	310	315
Glu Phe Leu Ser Phe Leu Leu Ser Pro Leu Glu Leu Ser Asp Ser	320	325	330
Glu Pro Val Val Val Tyr Gly Met Asp Tyr Leu Gln Gln Val Ser	335	340	345

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Lys Lys Ser Cys Val Pro Arg Trp Gln Thr Cys Ile Ser Asn Thr	395	400	405
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Met Thr Pro Gln Thr Val Asn Ala Tyr Tyr Leu Pro Thr Lys Asn	530	535	540
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Arg Asn His Pro Lys Ala Leu Asn Phe Gly Gly Ile Gly Val Val	560	565	570
Met Gly His Glu Leu Thr His Ala Phe Asp Asp Gln Gly Arg Glu	575	580	585
Tyr Asp Lys Glu Gly Asn Leu Arg Pro Trp Trp Gln Asn Glu Ser	590	595	600
Leu Ala Ala Phe Arg Asn His Thr Ala Cys Met Glu Glu Gln Tyr	605	610	615
Asn Gln Tyr Gln Val Asn Gly Glu Arg Leu Asn Gly Arg Gln Thr	620	625	630

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Glu	Gly	Leu	Val	Thr	Asp	Pro	His	Ser	Pro	Ala	Arg	Phe	Arg	Val	695	700	705
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Trp

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<211> 4308

<212> DNA

<213> Homo sapiens

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<223> unknown base

<400> 527

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tgtggcacag acccaatcct 20

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aagcttctgt tcaatcccag cgtcc 26

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<210> 581

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<210> 597

<211> 25

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<223> Synthetic oligonucleotide probe

<400> 597

tccaacaacc attttcctct ggtcc 25

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<400> 598

aagcagtagc cattaacaag tca 23

<210> 599

<211> 20

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<223> Synthetic oligonucleotide probe

<400> 599

caagcgtcca ggtttattga 20

<210> 600

<211> 20

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ccggctgggt ctcaactcctc c 21

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<213> Homo Sapien

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accacccac caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaatc 200
ctgtggcgcg ccgcctggtt cccgggaaga ctgccagca ccagggggtg 250
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 <211> 352
 <212> PRT
 <213> Homo Sapien

<400> 612
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 1 5 10 15
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 20 25 30
 Pro Ala Gly Gln Ser Val Asp Phe Pro Trp Ala Ala Val Asp Asn
 35 40 45
 Met Met Val Arg Lys Gly Asp Thr Ala Val Leu Arg Cys Tyr Leu
 50 55 60
 Glu Asp Gly Ala Ser Lys Gly Ala Trp Leu Asn Arg Ser Ser Ile
 65 70 75
 Ile Phe Ala Gly Gly Asp Lys Trp Ser Val Asp Pro Arg Val Ser
 80 85 90
 Ile Ser Thr Leu Asn Lys Arg Asp Tyr Ser Leu Gln Ile Gln Asn
 95 100 105
 Val Asp Val Thr Asp Asp Gly Pro Tyr Thr Cys Ser Val Gln Thr

110	115	120
Gln His Thr Pro Arg Thr Met Gln Val	His Leu Thr Val Gln Val	
125	130	135
Pro Pro Lys Ile Tyr Asp Ile Ser Asn	Asp Met Thr Val Asn Glu	
140	145	150
Gly Thr Asn Val Thr Leu Thr Cys Leu	Ala Thr Gly Lys Pro Glu	
155	160	165
Pro Ser Ile Ser Trp Arg His Ile Ser	Pro Ser Ala Lys Pro Phe	
170	175	180
Glu Asn Gly Gln Tyr Leu Asp Ile Tyr	Gly Ile Thr Arg Asp Gln	
185	190	195
Ala Gly Glu Tyr Glu Cys Ser Ala Glu	Asn Ala Val Ser Phe Pro	
200	205	210
Asp Val Arg Lys Val Lys Val Val Val	Asn Phe Ala Pro Thr Ile	
215	220	225
Gln Glu Ile Lys Ser Gly Thr Val Thr	Pro Gly Arg Ser Gly Leu	
230	235	240
Ile Arg Cys Glu Gly Ala Gly Val Pro	Pro Pro Ala Phe Glu Trp	
245	250	255
Tyr Lys Gly Glu Lys Lys Leu Phe Asn	Gly Gln Gln Gly Ile Ile	
260	265	270
Ile Gln Asn Phe Ser Thr Arg Ser Ile	Leu Thr Val Thr Asn Val	
275	280	285
Thr Gln Glu His Phe Gly Asn Tyr Thr	Cys Val Ala Ala Asn Lys	
290	295	300
Leu Gly Thr Thr Asn Ala Ser Leu Pro	Leu Asn Pro Pro Ser Thr	
305	310	315
Ala Gln Tyr Gly Ile Thr Gly Ser Ala	Asp Val Leu Phe Ser Cys	
320	325	330
Trp Tyr Leu Val Leu Thr Leu Ser Ser	Phe Thr Ser Ile Phe Tyr	
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Leu Lys Asn Ala Ile Leu Gln		
350		

<210> 613

<211> 1797

<212> DNA

<213> Homo Sapien

<400> 613

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ctgcttttca ccaaattgca atggagcctt tcgaaatcaa tgttccaaag 200
cccaagagga gaaatggggt gaactttctcc ctagctgtgg tggatcatcta 250
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gaagtttact acagtggtag ctgggggaca atttgcgatg acgagtggca 1450

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 <211> 520
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 <213> Homo Sapien

<400> 614

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Ile	Asn	Val	Pro	Lys	Pro	Lys	Arg	Arg	Asn	Gly	Val	Asn	Phe	Ser	35	40	45	
Leu	Ala	Val	Val	Val	Ile	Tyr	Leu	Ile	Leu	Leu	Thr	Ala	Gly	Ala	50	55	60	
Gly	Leu	Leu	Val	Val	Gln	Val	Leu	Asn	Leu	Gln	Ala	Arg	Leu	Arg	65	70	75	
Val	Leu	Glu	Met	Tyr	Phe	Leu	Asn	Asp	Thr	Leu	Ala	Ala	Glu	Asp	80	85	90	
Ser	Pro	Ser	Phe	Ser	Leu	Leu	Gln	Ser	Ala	His	Pro	Gly	Glu	His	95	100	105	
Leu	Ala	Gln	Gly	Ala	Ser	Arg	Leu	Gln	Val	Leu	Gln	Ala	Gln	Leu	110	115	120	
Thr	Trp	Val	Arg	Val	Ser	His	Glu	His	Leu	Leu	Gln	Arg	Val	Asp	125	130	135	
Asn	Phe	Thr	Gln	Asn	Pro	Gly	Met	Phe	Arg	Ile	Lys	Gly	Glu	Gln	140	145	150	
Gly	Ala	Pro	Gly	Leu	Gln	Gly	His	Lys	Gly	Ala	Met	Gly	Met	Pro	155	160	165	
Gly	Ala	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Ala	Glu	Lys	Gly	Ala	Lys	170	175	180	
Gly	Ala	Met	Gly	Arg	Asp	Gly	Ala	Thr	Gly	Pro	Ser	Gly	Pro	Gln				

185	190	195
Gly Pro Pro Gly Val Lys Gly Glu Ala	Gly Leu Gln Gly Pro Gln	
200	205	210
Gly Ala Pro Gly Lys Gln Gly Ala Thr	Gly Thr Pro Gly Pro Gln	
215	220	225
Gly Glu Lys Gly Ser Lys Gly Asp Gly	Gly Leu Ile Gly Pro Lys	
230	235	240
Gly Glu Thr Gly Thr Lys Gly Glu Lys	Gly Asp Leu Gly Leu Pro	
245	250	255
Gly Ser Lys Gly Asp Arg Gly Met Lys	Gly Asp Ala Gly Val Met	
260	265	270
Gly Pro Pro Gly Ala Gln Gly Ser Lys	Gly Asp Phe Gly Arg Pro	
275	280	285
Gly Pro Pro Gly Leu Ala Gly Phe Pro	Gly Ala Lys Gly Asp Gln	
290	295	300
Gly Gln Pro Gly Leu Gln Gly Val Pro	Gly Pro Pro Gly Ala Val	
305	310	315
Gly His Pro Gly Ala Lys Gly Glu Pro	Gly Ser Ala Gly Ser Pro	
320	325	330
Gly Arg Ala Gly Leu Pro Gly Ser Pro	Gly Ser Pro Gly Ala Thr	
335	340	345
Gly Leu Lys Gly Ser Lys Gly Asp Thr	Gly Leu Gln Gly Gln Gln	
350	355	360
Gly Arg Lys Gly Glu Ser Gly Val Pro	Gly Pro Ala Gly Val Lys	
365	370	375
Gly Glu Gln Gly Ser Pro Gly Leu Ala	Gly Pro Lys Gly Ala Pro	
380	385	390
Gly Gln Ala Gly Gln Lys Gly Asp Gln	Gly Val Lys Gly Ser Ser	
395	400	405
Gly Glu Gln Gly Val Lys Gly Glu Lys	Gly Glu Arg Gly Glu Asn	
410	415	420
Ser Val Ser Val Arg Ile Val Gly Ser	Ser Asn Arg Gly Arg Ala	
425	430	435
Glu Val Tyr Tyr Ser Gly Thr Trp Gly	Thr Ile Cys Asp Asp Glu	
440	445	450
Trp Gln Asn Ser Asp Ala Ile Val Phe	Cys Arg Met Leu Gly Tyr	
455	460	465
Ser Lys Gly Arg Ala Leu Tyr Lys Val	Gly Ala Gly Thr Gly Gln	

470

475

480

Ile Trp Leu Asp Asn Val Gln Cys Arg Gly Thr Glu Ser Thr Leu
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Trp Ser Cys Thr Lys Asn Ser Trp Gly His His Asp Cys Ser His
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Glu Glu Asp Ala Gly Val Glu Cys Ser Val
 515 520

<210> 615

<211> 647

<212> DNA

<213> Homo Sapien

<400> 615

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atttaagaag catcctctgc caagacaaa aggaaagaag aaaaagggcc 150

aaaagccaaa atgaaactga tgggtacttgt ttccaccatt gggctaactt 200

tgctgctagg agttcaagcc atgcctgcaa atcgctctc ttgctacaga 250

aagatactaa aagatcacia ctgtcacaac cttccggaag gagtagctga 300

cctgacacag attgatgtca atgtccagga tcatttctgg gatgggaagg 350

gatgtgagat gatctgttac tgcaacttca gcgaattgct ctgctgcca 400

aaagacgttt tctttggacc aaagatctct ttctgtgattc cttgcaacaa 450

tcaatgagaa tcttcatgta ttctggagaa caccattcct gatttccac 500

aaactgcact acatcagtat aactgcattt ctagtttcta tatagtgcaa 550

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gttaaacaag tagtaataaa agttaattca atctaaaaaa aaaaaaa 647

<210> 616

<211> 98

<212> PRT

<213> Homo Sapien

<400> 616

Met Lys Leu Met Val Leu Val Phe Thr Ile Gly Leu Thr Leu Leu
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Leu Gly Val Gln Ala Met Pro Ala Asn Arg Leu Ser Cys Tyr Arg
 20 25 30

Lys Ile Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val
 35 40 45

Ala	Asp	Leu	Thr	Gln	Ile	Asp	Val	Asn	Val	Gln	Asp	His	Phe	Trp
				50					55					60
Asp	Gly	Lys	Gly	Cys	Glu	Met	Ile	Cys	Tyr	Cys	Asn	Phe	Ser	Glu
				65					70					75
Leu	Leu	Cys	Cys	Pro	Lys	Asp	Val	Phe	Phe	Gly	Pro	Lys	Ile	Ser
				80					85					90
Phe	Val	Ile	Pro	Cys	Asn	Asn	Gln							
				95										

<210> 617
 <211> 2558
 <212> DNA
 <213> Homo Sapien

<400> 617
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 accccgccgt ggtggttggg gggcgcgag tagagcagca gcacaggcgc 150
 ggggtcccggg aggcgggctc tgctcgccg gagatgtgga atctccttca 200
 cgaaaccgac tcggctgtgg ccaccgcgc cgcgccgcg tggtgtgcg 250
 ctggggcgct ggtgctggcg ggtggcttct ttctctcgg ctctctcttc 300
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<210> 618
 <211> 750
 <212> PRT
 <213> Homo Sapien

<400> 618
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 Arg Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly
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 Gly Phe Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser
 35 40 45
 Ser Asn Glu Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala
 50 55 60
 Phe Leu Asp Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu His
 65 70 75
 Asn Phe Thr Gln Ile Pro His Leu Ala Gly Thr Glu Gln Asn Phe
 80 85 90
 Gln Leu Ala Lys Gln Ile Gln Ser Gln Trp Lys Glu Phe Gly Leu
 95 100 105
 Asp Ser Val Glu Leu Ala His Tyr Asp Val Leu Leu Ser Tyr Pro
 110 115 120
 Asn Lys Thr His Pro Asn Tyr Ile Ser Ile Ile Asn Glu Asp Gly
 125 130 135
 Asn Glu Ile Phe Asn Thr Ser Leu Phe Glu Pro Pro Pro Pro Gly
 140 145 150
 Tyr Glu Asn Val Ser Asp Ile Val Pro Pro Phe Ser Ala Phe Ser
 155 160 165
 Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr Val Asn Tyr Ala
 170 175 180
 Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met Lys Ile Asn
 185 190 195
 Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val Phe Arg
 200 205 210

Gly Asn Lys Val	Lys Asn Ala Gln Leu	Ala Gly Ala Lys Gly	Val
215	220	225	
Ile Leu Tyr Ser	Asp Pro Ala Asp Tyr	Phe Ala Pro Gly Val	Lys
230	235	240	
Ser Tyr Pro Asp	Gly Trp Asn Leu Pro	Gly Gly Gly Val Gln	Arg
245	250	255	
Gly Asn Ile Leu	Asn Leu Asn Gly Ala	Gly Asp Pro Leu Thr	Pro
260	265	270	
Gly Tyr Pro Ala	Asn Glu Tyr Ala Tyr	Arg Arg Gly Ile Ala	Glu
275	280	285	
Ala Val Gly Leu	Pro Ser Ile Pro Val	His Pro Ile Gly Tyr	Tyr
290	295	300	
Asp Ala Gln Lys	Leu Leu Glu Lys Met	Gly Gly Ser Ala Pro	Pro
305	310	315	
Asp Ser Ser Trp	Arg Gly Ser Leu Lys	Val Pro Tyr Asn Val	Gly
320	325	330	
Pro Gly Phe Thr	Gly Asn Phe Ser Thr	Gln Lys Val Lys Met	His
335	340	345	
Ile His Ser Thr	Asn Glu Val Thr Arg	Ile Tyr Asn Val Ile	Gly
350	355	360	
Thr Leu Arg Gly	Ala Val Glu Pro Asp	Arg Tyr Val Ile Leu	Gly
365	370	375	
Gly His Arg Asp	Ser Trp Val Phe Gly	Gly Ile Asp Pro Gln	Ser
380	385	390	
Gly Ala Ala Val	Val His Glu Ile Val	Arg Ser Phe Gly Thr	Leu
395	400	405	
Lys Lys Glu Gly	Trp Arg Pro Arg Arg	Thr Ile Leu Phe Ala	Ser
410	415	420	
Trp Asp Ala Glu	Glu Phe Gly Leu Leu	Gly Ser Thr Glu Trp	Ala
425	430	435	
Glu Glu Asn Ser	Arg Leu Leu Gln Glu	Arg Gly Val Ala Tyr	Ile
440	445	450	
Asn Ala Asp Ser	Ser Ile Glu Gly Asn	Tyr Thr Leu Arg Val	Asp
455	460	465	
Cys Thr Pro Leu	Met Tyr Ser Leu Val	His Asn Leu Thr Lys	Glu
470	475	480	
Leu Lys Ser Pro	Asp Glu Gly Phe Glu	Gly Lys Ser Leu Tyr	Glu
485	490	495	

Ser Trp Thr Lys	Lys Ser Pro Ser Pro	Glu Phe Ser Gly Met	Pro
500		505	510
Arg Ile Ser Lys	Leu Gly Ser Gly Asn	Asp Phe Glu Val Phe	Phe
515		520	525
Gln Arg Leu Gly	Ile Ala Ser Gly Arg	Ala Arg Tyr Thr Lys	Asn
530		535	540
Trp Glu Thr Asn	Lys Phe Ser Gly Tyr	Pro Leu Tyr His Ser	Val
545		550	555
Tyr Glu Thr Tyr	Glu Leu Val Glu Lys	Phe Tyr Asp Pro Met	Phe
560		565	570
Lys Tyr His Leu	Thr Val Ala Gln Val	Arg Gly Gly Met Val	Phe
575		580	585
Glu Leu Ala Asn	Ser Ile Val Leu Pro	Phe Asp Cys Arg Asp	Tyr
590		595	600
Ala Val Val Leu	Arg Lys Tyr Ala Asp	Lys Ile Tyr Ser Ile	Ser
605		610	615
Met Lys His Pro	Gln Glu Met Lys Thr	Tyr Ser Val Ser Phe	Asp
620		625	630
Ser Leu Phe Ser	Ala Val Lys Asn Phe	Thr Glu Ile Ala Ser	Lys
635		640	645
Phe Ser Glu Arg	Leu Gln Asp Phe Asp	Lys Ser Asn Pro Ile	Val
650		655	660
Leu Arg Met Met	Asn Asp Gln Leu Met	Phe Leu Glu Arg Ala	Phe
665		670	675
Ile Asp Pro Leu	Gly Leu Pro Asp Arg	Pro Phe Tyr Arg His	Val
680		685	690
Ile Tyr Ala Pro	Ser Ser His Asn Lys	Tyr Ala Gly Glu Ser	Phe
695		700	705
Pro Gly Ile Tyr	Asp Ala Leu Phe Asp	Ile Glu Ser Lys Val	Asp
710		715	720
Pro Ser Lys Ala	Trp Gly Glu Val Lys	Arg Gln Ile Tyr Val	Ala
725		730	735
Ala Phe Thr Val	Gln Ala Ala Ala Glu	Thr Leu Ser Glu Val	Ala
740		745	750

<210> 619

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 619

agatgtgaag gtgcaggtgt gccg 24

<210> 620

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 620

gaacatcagc gctcccgta attcc 25

<210> 621

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 621

ccagcctttg aatggtacaa aggagagaag aagctcttca atggcc 46

<210> 622

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 622

ccaaactcac ccagtgagtg tgagc 25

<210> 623

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 623

tgggaaatca ggaatggtgt tctcc 25

<210> 624

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide probe

<400> 624

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